

Original Research Article

Identification and immune recognition of viral epitopes of West Nile Virus envelope glycoprotein and their potentials of acting as peptide vaccine

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Abstract: West Nile virus (WNV) is a small, enveloped, mosquito transmitted virus with a positive sense, 11 kb RNA genome. It was first isolated in 1937 from a woman with an undiagnosed febrile illness in the West Nile district of Uganda, WNV is currently the most widely distributed arbovirus in the world, occurring in all continents except Antarctica, there are no clinically approved vaccines or antiviral drugs, thus, the aim of this study is to analyze envelope glycoprotein variants using in silico approaches looking for conservancy, which is further studied to predict all potential epitopes that can be used after in vitro and in vivo confirmation as a therapeutic peptide vaccine. Total of 149 envelope glycoprotein variants retrieved from NCBI database were introduced to IEDB conservancy tool, to select the highly conserved regions for epitopes prediction. By means of IEDB analysis resource B and T cell epitopes were predicted and population coverage was calculated. Three epitopes were proposed for international therapeutic peptide vaccine for B cell (DLSTKAACPTMGEAHNDKADPAFV, YGEVTVDCEPRSGIDTN and PVEFSSNTVKL). Regarding T cell, RSYCYLATV epitope was highly recommended as therapeutic peptide vaccine to interact with MHC class I along with five other epitopes that showed good population coverage against whole world population. Two epitopes showed high affinity to interact with MHC class II alleles (IKYEVAIFV and WFMDLNLPW). Epitopes defined by methods such as the one described here are likely to contribute substantially to the development of new in vivo and in vitro research, diagnostic and vaccines for WNV and other emerging infectious diseases.

Keywords: WNV, Peptide vaccine, Immune Epitope Database IEDB, Epitopes and Vaccine.

INTRODUCTION

West Nile virus (WNV) is a small, enveloped, mosquito transmitted virus with a positive sense, 11 kb RNA genome. It is a member of the Japanese encephalitis (JE) serocomplex of the family Flaviviridae, genus Flavivirus and related to other arthropod-borne viruses that cause human disease globally including dengue, yellow fever, and Zika viruses [1 -4].

WNV is currently the most widely distributed arbovirus in the world, occurring in all continents except Antarctica. It was first isolated in 1937 from a woman with an undiagnosed febrile illness in the West Nile district of Uganda [5, 6]. Then in a (1939-1940) serosurvey widespread human seropositivity for WNV in Uganda, Sudan, the current Democratic Republic of the Congo and Kenya was found [7, 8]. It wasn't isolated again until 1950 in Egypt and the upper Nile delta, then it continued to circulate in northern and sub-

Saharan Africa throughout the late 20th and early 21st century, causing outbreaks in Algeria, Morocco, Tunisia, the Democratic Republic of the Congo and South Africa along with sporadic cases and seropositivity in humans distributed throughout the continent. WNV invasion wasn't confined to Africa only; as many cases and epidemics were reported in southern and eastern Asia including India, Malaysia and Cambodia among others [8]. The first confirmed human cases of WNV in China were reported in 2013 but occurred during 2004 outbreak of fever and neurological disease in Xinjiang province in northwestern China [9, 10]. Europe also have been engaged in the WNV epidemics since 1960s and mainly in central and south-eastern regions in which infections and virulence have recently increased [11-13]. Since WNV crossed the Atlantic Ocean to the western hemisphere it imposed a major public health concern in the United States, where it has become endemic causing recurring outbreaks for many consecutive years since

1999. By 2004, WNV had been detected in United States, it was controlled for a while before it burst again in 2012 [8, 14, 15]. As of January 12, 2016, all US states and the District of Columbia have reported West Nile virus infections in people, birds, or mosquitoes. Overall, 2,060 of West Nile human infection cases in US have been reported to CDC [16]. From US it progressed downward to the Southern America and imparted many sporadic as well as epidemics since 2004 [17].

During the last 16 years, increasing numbers of WNV outbreaks have been associated with the appearance of more neuroinvasive strains and higher human fatalities. In 2012, WNV cases were reported worldwide, with more than 50 cases reported in Italy, Israel, Russia, Serbia and Tunisia. Greece alone reported 167 cases. In 2015, 108 cases of West Nile fever in humans have been reported in the EU, 125 in Israel, 39 in the Russian Federation, 28 in Serbia and one case in Palestine. As of the 23th June, no human cases of West Nile fever have been reported in the EU but six cases were reported in Israel [18, 19].

Phylogenetic analysis describes five distinct WNV lineages, among which lineage 1 is the most virulent as it is responsible for the fatal neuroinvasive disease in humans and animals and its strains are found in North America, Israel, Africa, Asia, the Middle East, Europe and Australia [2, 20].

Mosquito Species in the genus *Culex* appear to be the main vectors implicated in the avian amplification cycle of WNV. Nevertheless, reports of transmission through blood transfusions, organ donations and from mother to neonate during childbirth or breastfeeding were discovered. Guillain-Barré syndrome has been reported with WNV infections which is mainly associated with many neurological manifestations as encephalitis, meningitis, flaccid paralysis, persistent neurologic sequelae and possibly death, particularly in the elderly and

immunocompromised individuals [2-23]. Currently, there is neither specific therapy for treatment nor vaccine has been approved for prevention of WNV infection in humans, protection is only achieved by controlling mosquitoes and avoiding mosquito bites [22]. Thus, development of a vaccine is an obvious priority as to enhance prevention and that hasn't accomplished yet.

Surface or envelope proteins of the virus represent the most antigenic molecular parts and often considered as good candidates for immunization. They are important for vaccine development as they are involved in the virus attachment, internalization and resemble the primary targets of adaptive immune response [24-26]. Several attempts for developing vaccines are encouraged by many institutions and number of technologies have been involved including live attenuated vaccine, DNA-based vaccine, chimeric vaccine, mRNA vaccine, influenza virus expressing WNV E protein, Newcastle disease virus expressing WNV premembrane/envelope (PrM/E) proteins and other approaches related to vector control [22, 27,28].

The aim of this study is to analyze envelope glycoprotein E of all West Nile Virus variants available sequences using in silico approaches looking for conservancy, which will then further studied to predict all potential B and T cell epitopes that can be used after in vitro and in vivo confirmation as a therapeutic peptide vaccine or diagnostic screening protocol.

MATERIALS AND METHODS

Protein Sequences retrieval

The complete protein sequences of envelope protein of WNV were retrieved from the NCBI protein database (<http://www.ncbi.nlm.nih.gov/protein/>). A total of 146 protein variants were retrieved in June 2016. These retrieved strains were collected from different countries listed with their accession numbers in Table 1.

Table-1: West Nile E protein variants and their date and area of collection

Accession NO	Country of collection	Date of collection
YP_001527880*	USA	N.A**
ABZ10681	Israel	N.A
ABZ10683	Israel	N.A
AAM70028	N.A	N.A
ABZ10680	Israel	N.A
ABZ10679	Israel	N.A
ABZ10678	Israel	N.A
AJW67513	Colombia	2012
AJW67514	Colombia	2012
AGM61320	China	2011
AGM61322	China	2011
AGM61323	China	2011
AGM61324	China	2011
AHV83441	Senegal	1990
AHV83442	Senegal	1993
AHV83443	Senegal	1992
AHV83444	Senegal	1993
AHI48937	USA	2010

AHI48938	USA	2010
AHI48939	USA	2010
AHI48940	USA	2010
AHI48941	USA	2010
AHI48942	USA	2010
AHI48943	USA	2010
AHI48944	UAS	2010
AHI48945	UAS	2010
AHI48946	UAS	2010
AHI48947	UAS	2010
AHI48948	UAS	2010
ADR30044	Italy	2009
ADR30045	Italy	2009
ADR30046	Italy	2009
ADR30047	Italy	2009
ADR30048	Italy	2009
ADR30049	Italy	2009
AAT11534	USA	N.A
AAT11535	USA	N.A
AAT11536	USA	N.A
AAT11537	USA	N.A
AAT11538	USA	N.A
AAT11539	USA	N.A
AAT11540	USA	N.A
AAT11541	USA	N.A
AAT11542	USA	N.A
AAT11543	USA	N.A
AAT11544	USA	N.A
AAT11545	USA	N.A
AAT11546	USA	N.A
AAT11547	USA	N.A
AAT11548	USA	N.A
AAT11550	USA	N.A
AAT11551	USA	N.A
AAT11552	USA	N.A
AAT11553	USA	N.A
AAD31720	Kenya	N.A
AAR17559	N.A	N.A
AAR17560	N.A	N.A
AAR17561	N.A	N.A
AAR17562	N.A	N.A
AAR17563	N.A	N.A
AAR17564	N.A	N.A
AAR17565	N.A	N.A
AAR17566	N.A	N.A
AAR17567	N.A	N.A
AAR17568	N.A	N.A
AAR17569	N.A	N.A
AAR17570	N.A	N.A
AAR17571	N.A	N.A
AAR17572	N.A	N.A
AAR17573	N.A	N.A
AAR17574	N.A	N.A
AAR17575	N.A	N.A
AGU04094	N.A	N.A
AJM45689	N.A	N.A
ACP75626	N.A	N.A
CAM90884	N.A	N.A
ABH06911	USA	2004
ABH06912	USA	2004
ABH06913	USA	2004
ABH06914	USA	2004
ABH06915	USA	2004
ABH06916	USA	2004
ABH06917	USA	2004
ABH06918	USA	2004
ABH06919	USA	2004
ABH06920	USA	2004
ABH06921	USA	2004
ABH06922	USA	2004
ABH06923	USA	2004

ABH06924	USA	2004
ABH06925	USA	2004
ABH06926	USA	2004
ABH06927	USA	2004
ABH06928	USA	2004
ABH06929	USA	2004
ABH06930	USA	2004
ABH06931	USA	2005
ABH06932	USA	2005
ABH06933	USA	2005
ABH06934	USA	2005
ABH06935	USA	2005
ABH06936	USA	2005
ABH06937	USA	2005
ABH06938	USA	2005
ABH06939	USA	2005
ABH06940	USA	2005
ABH06941	USA	2005
ABH06942	USA	2005
ABH06943	USA	2005
ABH06944	USA	2005
ABH06945	USA	2005
ABH06946	USA	2005
ABH06947	USA	2005
ABH06948	USA	2005
ABH06949	USA	2005
ABH06950	USA	2005
AAK62756	N.A	N.A
AAK62757	N.A	N.A
AAK62758	N.A	N.A
AAK62759	N.A	N.A
AAK62760	N.A	N.A
AAK62761	N.A	N.A
AAK62762	N.A	N.A
AAK62763	N.A	N.A
AAK62764	N.A	N.A
AAK62765	N.A	N.A
AAK62766	N.A	N.A
AAR17542	N.A	N.A
AAR17543	N.A	N.A
AAR17544	N.A	N.A
AAR17545	N.A	N.A
AAR17546	N.A	N.A
AAR17547	N.A	N.A
AAR17548	N.A	N.A
AAR17549	N.A	N.A
AAR17550	N.A	N.A
AAR17551	N.A	N.A
AAR17552	N.A	N.A
AAR17553	N.A	N.A
AAR17555	N.A	N.A
AAR17556	N.A	N.A
AAR17557	N.A	N.A
AAR17558	N.A	N.A
AAR17559	N.A	N.A

* Ref sequence.

**not available.

Conservancy analysis

The degree of conservancy was measured using immune epitope conservancy analysis tool (http://tools.iedb.org/tools/conservancy/iedb_input), all predicted B and T cell epitopes were subjected to this analysis. Epitopes with conservancy equal or higher than 90% were proposed as best candidates[29].

B-cell Epitope Prediction

The B-cell epitope prediction was performed using <http://tools.iedb.org/bcell/> using three parameters; Firstly, BepiPred from immune epitope database [30] was used for linear B-cell epitopes prediction from the highly conserved regions with a threshold value of - 0.01. Secondly, Emini surface accessibility prediction tool of the immune epitope data base [31], the surface accessible epitopes were

predicted from the highly conserved regions holding the default threshold value 1.000 or higher. Lastly, Kolaskar and Tongaonkar antigenicity method was used to determine the antigenic sites with a default threshold value of 1.036 [32].

T-cell Epitope prediction

Initially, the amino acid sequence of the reference envelope protein of WNV was obtained from NCBI database, sequence was obtained in FASTA format. For the prediction of MHC class-I epitopes; IEDB MHC I binding analysis tool was used [33]. The sequence was submitted in FASTA format and with specific selected alleles. The epitopes were predicted for different alleles of MHC class-I. The predicted epitopes were in the form of nine amino acid peptides. For the prediction of MHC class-II epitopes same IEDB analysis tool was used but with different parameters. All predicted epitopes were in the form of 15 amino acid peptide with 9mer core peptide sequences. IEDB provides a collection of tools for the prediction and analysis of epitopes for MHC class I and MHC class II. Epitopes was predicted utilizing alleles data set. These small sequence epitopes were obtained from the IEDB analysis tool by using the artificial neural network method(ANN) [34 -39].

Population coverage

MHCI and MHCII binding epitopes were assessed to estimate epitope-allele coverage among all populations in the world using IEDB tool (<http://www.iedb.org/>) [40].

Homology Modeling

A Three Dimensional structure protein model was created using protein structure modeling server

SWISSMODEL and UCSF Chimera (version 1.8) package available at <http://www.cgl.ucsf.edu/cimera>) was used for visualization of the selected epitopes in the structural level [41, 42].

RESULTS:

Prediction of B-cell epitopes

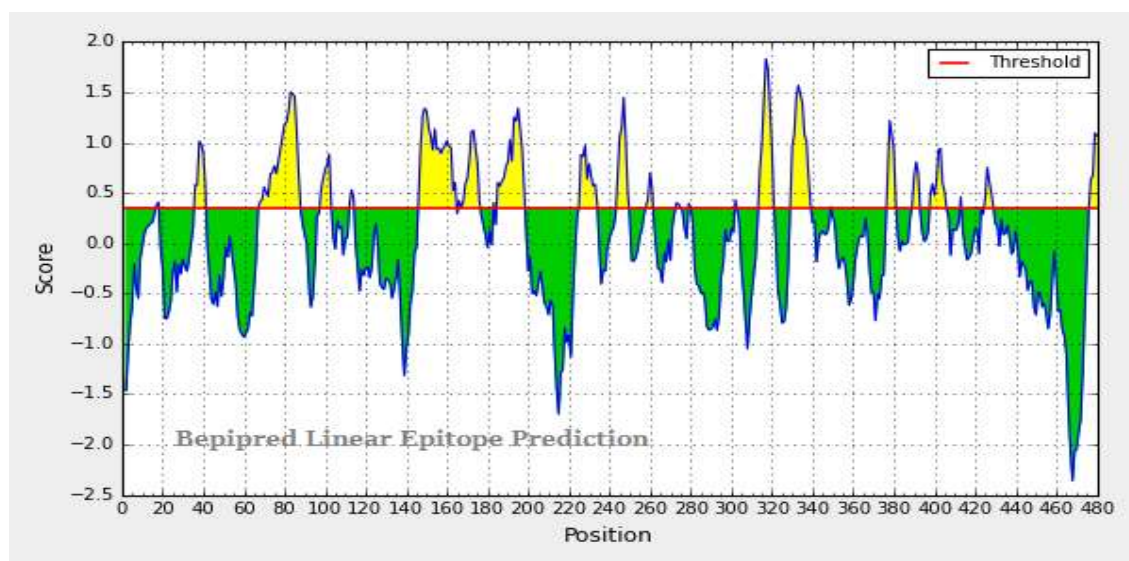
Envelope glycoprotein was subjected to Bepipred linear epitope prediction, Emini surface accessibility and Kolaskar and Tongaonkar antigenicity prediction methods in IEDB, figure (1).

In Bepipred Linear Epitope Prediction method; the average binders score of envelope glycoprotein to B cell was -0.01, all values equal or greater than the default threshold -0.01 were predicted to be potential B cell binders.

In Emini surface accessibility prediction; the average surface accessibility areas of the protein was scored as 1.000, all values equal or greater than the default threshold 1.0 were regarded potentially in the surface.

The default threshold of antigenicity of the protein was 1.036; all values greater than 1.036 were considered as potential antigenic determinants.

Three >90% conserved epitopes out of 24 epitopes had succeeded all prediction methods, epitope YGEVTVDCPRSGIDTN was found to have the highest conservancy score as 95.86% among retrieved variants, The result is summarized in table (2) and proposed epitopes are shown in figure (2) at the structural level of the envelope protein.



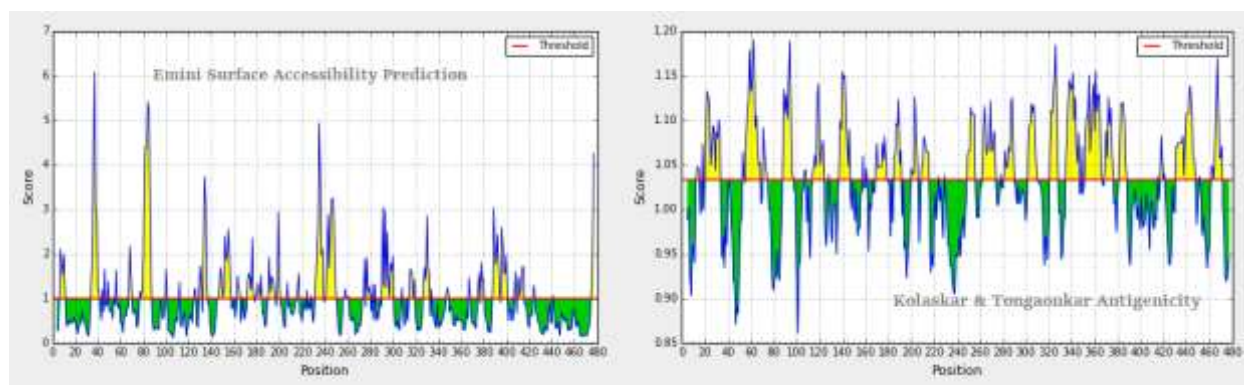


Fig-1: Prediction of B-cell epitopes by different scales Yellow areas above threshold (red line) are proposed to be a part of B cell epitope. While green areas are not.

Table-2: List of B- cell epitopes predicted by different scales

Epitope sequence	Epitope length	Eimini Surface Accessibility score ^a	Kloaskar & Tongaonkar Antigenicity score ^b
FLEGVSGA	8	0.263	1.05
MSKDKPTI	8	2.991	0.961
DLSTKAACPTMGEAHNDKRAPAFV*	25	2.488	1.007
VVDRGWGNG	9	0.532	0.977
GLF	3	0.391	1.072
KGSIDT	6	1.401	0.957
YGEVTVDCPRSGIDTN*	17	1.453	1.013
PWSSAGSTVWR	11	1.075	0.999
MEFEPPHATKQ	11	5.891	0.96
LGSQEGAL	8	0.584	1.024
PVEFSSNTVKL*	11	1.094	1.06
LKGTTYGV	8	0.845	1.036
GTPADTGHGT	10	1.547	0.945
YTGTDPCKVPIS	13	0.822	1.047
VASLNDLTP	9	0.738	1.064
SVATA	5	0.553	1.086
EPPFGDS	7	2.066	0.975
VGRGEQQINHHWHKSGSIGKA	22	2.378	0.995
TTTLKG	6	1.534	0.963
AAL	3	0.466	1.126
DTAWDFGSV	9	0.656	0.995
GVFTS	5	0.464	1.054
ARD	3	1.83	0.934

¹threshold :1.000² threshold : 1.036

* proposed epitopes

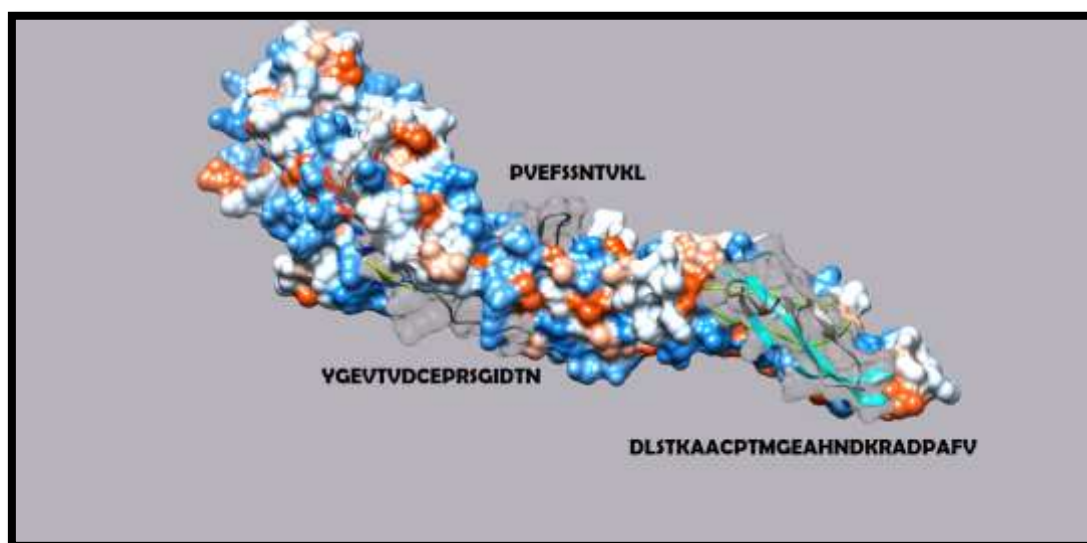


Fig-2: proposed B-Cell Epitopes

Proposed epitopes of B cell that are >90% conserved in all retrieved Envelope glycoprotein in the structural level.

Prediction of cytotoxic T cells epitopes and interaction with MHC Class I

Based on Artificial Neural Network (ANN) with $ic50 \leq 200$ and more than 90% conservancy 97

epitopes were predicted to interact with different MHC I alleles. The epitope TPAAPSYTL showed high affinity to interact with 5 alleles while RSYCYLATV interacted with 4 alleles including HLA-A*02:01. All epitopes and their corresponding MHC-1 alleles are shown in Table (3) Figure (3) displays epitopes in the structural level.

Table-3: List of epitopes that have binding affinity with the MHC Class I alleles

Epitope	Start	End	Allele	Percentile rank	Ann_ic50*
AEVRSYCYL	54	62	HLA-B*40:01	0.3	13
			HLA-B*40:02	1.05	98
AFKFLGTPA	308	316	HLA-A*30:01	2.4	195
ALHQALAGA	261	269	HLA-A*02:06	5.5	141
ASLNDLTPV	344	352	HLA-A*02:06	1.25	23
			HLA-C*15:02	1.35	122
ATANAKVLI	365	373	HLA-A*68:02	2.7	99
ATKQSVIAL	247	255	HLA-A*30:01	1.9	31
AVGGVLLFL	487	495	HLA-A*02:06	4	89
AVHQVFQGA	441	449	HLA-A*30:01	1.9	120
CAKFACSTK	116	124	HLA-A*68:01	1.3	60
			HLA-A*30:01	2	136
CYLATVSDL	60	68	HLA-A*23:01	0.55	80
			HLA-A*24:02	0.75	134
DSCVTIMSK	28	36	HLA-A*68:01	1.6	64
			HLA-A*11:01	2	188
DTAWDFGSV	423	431	HLA-A*68:02	0.3	6
EAANLAEVR	49	57	HLA-A*68:01	0.2	8
EVTVDCEPR	185	193	HLA-A*68:01	0.35	15
FLAVGGVLL	485	493	HLA-A*02:01	1.3	36
			HLA-A*02:06	3.05	71
FLVHREWFM	211	219	HLA-A*02:01	0.8	11
			HLA-A*02:06	1.05	17
FVSVATANA	361	369	HLA-A*68:02	1.1	29
			HLA-A*02:06	5.65	170
GEQQINHHW	389	397	HLA-B*44:02	0.15	21
GHLKCRVKM	284	292	HLA-C*07:01	41.6	177
GIDTNAYYV	195	203	HLA-A*02:01	1.4	35
			HLA-A*02:06	2.6	59
GMSWITQGL	456	464	HLA-A*02:01	2.3	50
GRLVTVNPF	353	361	HLA-B*27:05	0.5	88
GTKTFLVHR	207	215	HLA-A*31:01	0.25	5
			HLA-A*68:01	1.45	61
			HLA-A*30:01	5.7	73
GTTYGVCSK	299	307	HLA-A*11:01	1.1	47
			HLA-A*68:01	2	96
			HLA-A*30:01	2.7	79
GTVVLELQY	321	329	HLA-A*29:02	0.45	18
HQVFQGAFR	443	451	HLA-A*31:01	0.95	32
			HLA-A*68:01	2.2	100
IKYEVAIFV	135	143	HLA-A*02:06	3.15	100
KENIKYEVA	132	140	HLA-B*40:02	0.8	86
KTFLVHREW	209	217	HLA-B*57:01	0.1	13
			HLA-A*32:01	0.2	8
			HLA-B*58:01	0.2	9
LAALGDTAW	418	426	HLA-B*53:01	0.3	49
			HLA-B*58:01	0.3	11
			HLA-B*57:01	0.5	134
			HLA-B*35:01	1.2	51
LAEVRSYCY	53	61	HLA-B*35:01	1	37
LAGAIPVEF	266	274	HLA-B*35:01	1	24
			HLA-B*58:01	1.3	140
LAVGGVLLF	486	494	HLA-B*58:01	0.5	27
			HLA-B*53:01	0.6	107
			HLA-B*35:01	0.6	18
			HLA-B*15:01	1.3	71
			HLA-A*29:02	2.15	182
LEGDSCVTI	25	33	HLA-B*40:01	1.05	79

LEGVSGATW	12	20	HLA-B*44:02	0.2	59
LHQALAGAI	262	270	HLA-B*39:01	1.15	73
LLGALLLWM	464	472	HLA-A*02:01	2.9	176
LLLWMGINA	468	476	HLA-A*02:01	2.3	135
LLWMGINAR	469	477	HLA-A*31:01	1.3	63
LPWSSAGST	223	231	HLA-B*07:02	0.8	46
LTFLAVGGV	483	491	HLA-A*68:02	0.5	11
			HLA-A*02:06	4.3	106
LTSGHLKCR	281	289	HLA-A*68:01	2.05	144
LVLEGDSCV	23	31	HLA-A*02:06	1.15	18
MEANLANAEV	48	56	HLA-B*40:02	0.85	59
			HLA-A*68:02	1.9	76
			HLA-A*02:06	2.95	87
MEFEPPHAT	240	248	HLA-B*40:02	0.5	47
			HLA-B*18:01	0.9	58
MMNMEAANL	45	53	HLA-A*02:01	2.9	90
MSWITQGLL	457	465	HLA-B*58:01	2.3	122
MTVGTKTFL	204	212	HLA-A*68:02	0.6	9
			HLA-B*58:01	2.4	175
			HLA-C*15:02	4.8	92
			HLA-A*02:06	5.8	101
NARDRSIAL	475	483	HLA-B*08:01	0.3	28
			HLA-B*07:02	0.8	54
QALAGAIPV	264	272	HLA-A*02:06	2.45	58
			HLA-C*15:02	3.15	176
QEGALHQAL	258	266	HLA-B*40:01	0.6	29
			HLA-B*44:02	0.65	157
			HLA-B*40:02	1.3	34
QQINHHWHK	391	399	HLA-A*11:01	1.75	91
			HLA-A*31:01	2.1	76
RADPAFVCR	85	93	HLA-A*31:01	1.1	53
RETLMEFEE	236	244	HLA-B*40:02	1	124
REWFMDLNL	215	223	HLA-B*40:02	0.15	7
			HLA-B*40:01	0.25	12
RLVTVPFV	354	362	HLA-A*02:01	0.4	7
			HLA-A*02:06	0.65	8
			HLA-A*30:01	2.4	189
RSGIDTNAY	193	201	HLA-A*30:02	0.45	27
			HLA-B*15:01	2	174
RSIALTFLA	479	487	HLA-B*58:01	0.7	41
			HLA-A*30:01	1.9	120
			HLA-A*02:06	4.15	109
RSLFGGMSW	451	459	HLA-B*57:01	0.15	12
			HLA-B*58:01	0.2	5
			HLA-A*32:01	0.3	19
RSYCYLATV	57	65	HLA-C*15:02	0.15	16
			HLA-A*02:06	1	16
			HLA-A*02:01	3	83
			HLA-A*30:01	3.1	54
RTILKENIK	128	136	HLA-A*11:01	1.45	84
			HLA-A*30:01	2.3	172
RVKMEKLQL	289	297	HLA-A*30:01	1.3	57
SGIDTNAYY	194	202	HLA-A*30:02	0.6	66
			HLA-A*29:02	1.25	176
			HLA-B*15:01	2.6	150
SIALTFLAV	480	488	HLA-A*02:06	1.35	22
			HLA-A*68:02	2.7	154
			HLA-A*02:01	3	157
SITPAAPSY	168	176	HLA-A*30:02	0.4	30
			HLA-A*29:02	0.95	40
			HLA-B*15:01	2.2	193
			HLA-B*35:01	3.6	90
SLFGGMSWI	452	460	HLA-A*02:01	0.7	9
			HLA-A*02:06	3.75	47
SQEGALHQA	257	265	HLA-A*02:06	3.1	57
SSAGSTVWR	226	234	HLA-A*68:01	0.55	16
			HLA-A*11:01	1.8	191
			HLA-A*31:01	2.05	129
STKAACPTM	69	77	HLA-A*30:01	1.7	14
SVATANAKV	363	371	HLA-A*68:02	0.5	9
			HLA-A*02:06	5.6	169

SVGGVFTSV	430	438	HLA-A*68:02	0.8	30
			HLA-A*02:06	1.2	15
SVGKAVHQV	437	445	HLA-A*02:06	5.95	115
SYTLKLGEY	175	183	HLA-A*30:02	0.8	172
TFLVHREWF	210	218	HLA-A*23:01	0.45	78
TNAYYVMTV	198	206	HLA-A*68:02	0.9	22
TPAAPSYTL	170	178	HLA-B*39:01	0.2	10
			HLA-B*07:02	0.5	26
			HLA-B*35:03	0.8	165
			HLA-B*35:01	0.9	32
			HLA-A*68:02	4.7	62
TTTLKGAQR	409	417	HLA-A*68:01	0.55	27
			HLA-A*31:01	1.6	119
TTVESHGNY	147	155	HLA-A*26:01	0.25	13
			HLA-A*25:01	0.4	123
			HLA-A*29:02	1	51
TTYGVCSKA	300	308	HLA-A*68:02	1.3	36
TVGKTFLV	205	213	HLA-A*68:02	1	25
TVNPFVSV	357	365	HLA-A*68:02	1.9	69
TVSDLSTKA	64	72	HLA-A*68:02	2.7	70
TVWRNRETL	231	239	HLA-A*68:02	6	175
TYGVCSKAF	301	309	HLA-A*23:01	0.35	47
			HLA-A*24:02	0.4	100
VATANAKVL	364	372	HLA-C*15:02	1.4	159
VESHGNYST	149	157	HLA-B*40:02	0.8	125
VGKAVHQVF	438	446	HLA-B*15:01	2.3	95
VHREWFMDL	213	221	HLA-C*06:02	7.65	57
			HLA-C*07:01	11.75	47
VLIELEPPF	371	379	HLA-B*15:01	0.8	42
			HLA-A*02:06	3.75	87
VLLFLSVNV	491	499	HLA-A*02:01	0.7	16
			HLA-A*02:06	2.2	57
VPISSVASL	338	346	HLA-B*35:03	0.35	116
			HLA-B*07:02	0.4	17
			HLA-B*39:01	1.25	116
			HLA-B*35:01	2.4	88
VSVATANAK	362	370	HLA-A*11:01	1.35	66
VTNPFVSV	356	364	HLA-A*68:02	0.6	11
			HLA-A*02:06	0.85	11
WFMDLNLPW	217	225	HLA-B*53:01	0.6	90
			HLA-A*23:01	0.65	103
WITQGLLGA	459	467	HLA-A*02:06	4.25	63
WSSAGSTVW	225	233	HLA-B*58:01	0.2	5
			HLA-B*57:01	0.35	63
			HLA-B*15:01	3.2	131

* Inhibitory concentration needed to the binding; the lower is the better

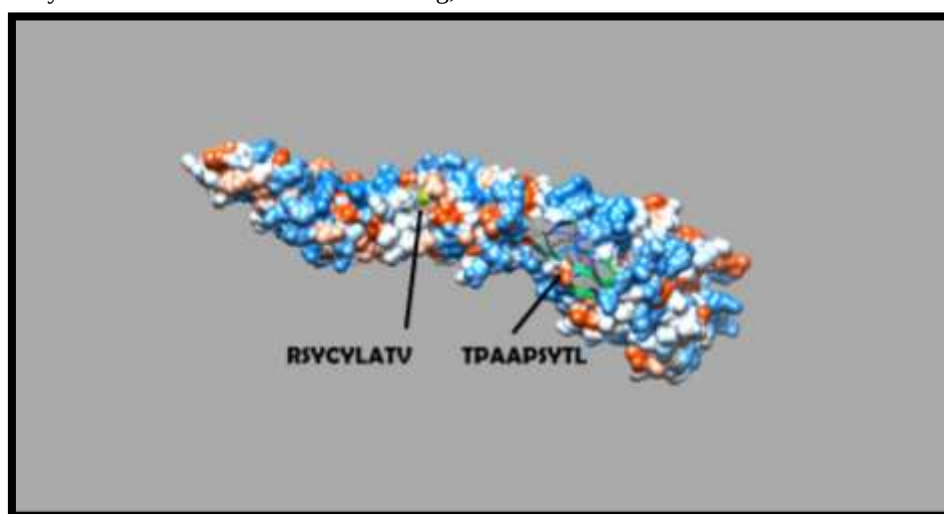


Fig-3: proposed T-Cell epitopes that interact with MHC Class I

Some proposed epitopes of MHC I that are >90% conserved in all Envelope glycoprotein strains in the structural level.

Prediction of Thelper cell epitopes and interaction with MHC Class II

The reference E protein was analyzed using IEDB MHC II binding prediction tool to predict T cell epitopes suggested interacting with different types of MHC Class II alleles. Based on Artificial Neural Network (ANN) with $ic50 \leq 1000$ and more than 90% conservancy 309 epitopes were predicted to interact with different MHC II alleles. [data not shown] from which the peptide (core) IKYEVAIFV had high affinity to interact with twenty two alleles; HLA-DRB1*09:01, HLA-DPA1*02:01, HLA-DPB1*05:01, HLA-DRB1*15:01, HLA-DRB1*04:01, HLA-DRB1*03:01, HLA-DRB1*07:01, HLA-DRB5*01:01,

HLA-DRB1*13:02, HLA-DPA1*01:03, HLA-DPB1*02:01, HLA-DRB3*01:01, HLA-DRB1*11:01, HLA-DPA1*02:01, HLA-DPB1*01:01, HLA-DRB1*04:05, HLA-DPA1*01:01, HLA-DPB1*04:01, HLA-DRB1*01:01, HLA-DQA1*05:01, HLA-DQB1*03:01, HLA-DRB4*01:01, while WFMDLNLPW had high affinity to interact with eighteen (HLA-DRB1*04:01, HLA-DRB3*01:01, HLA-DRB1*11:01, HLA-DRB1*03:01, HLA-DRB1*04:05, HLA-DRB1*15:01, HLA-DQA1*05:01, HLA-DQB1*02:01, HLA-DQA1*01:01, HLA-DQB1*05:01, HLA-DPA1*02:01, HLA-DPB1*01:01, HLA-DRB1*13:02, HLA-DPA1*01:03, HLA-DPB1*02:01, HLA-DRB1*07:01, HLA-DRB1*09:01, HLA-DRB1*01:01. The promiscuous epitopes and those which bind more than five different alleles are summarized in table 4. Figure 4 displays epitopes in the structural level.

Table-4: List of epitopes that have binding affinity with ≥ 5 Class II alleles

Epitope	Allele	Percentile rank	Peptide	Start	End	NN ic50*
CYLATVSDL	HLA-DQA1*04:01/DQB1*04:02	0.45	AEVRSYCYLATVSDL	54	68	549.8
	HLA-DPA1*03:01/DPB1*04:02	6.06	SYCYLATVSDLSTKA	58	72	86.9
	HLA-DPA1*03:01/DPB1*04:02	7.17	YCYLATVSDLSTKAA	59	73	93.3
	HLA-DQA1*04:01/DQB1*04:02	0.43	EVRSYCYLATVSDLS	55	69	593.4
	HLA-DPA1*03:01/DPB1*04:02	5.17	RSYCYLATVSDLSTK	57	71	108.5
	HLA-DQA1*04:01/DQB1*04:02	0.42	VRSYCYLATVSDLST	56	70	703.7
	HLA-DPA1*01:03/DPB1*02:01	4.95	AEVRSYCYLATVSDL	54	68	182.8
	HLA-DPA1*03:01/DPB1*04:02	5.26	VRSYCYLATVSDLST	56	70	160.9
	HLA-DQA1*04:01/DQB1*04:02	0.43	RSYCYLATVSDLSTK	57	71	997.5
	HLA-DPA1*03:01/DPB1*04:02	3.82	EVRSYCYLATVSDLS	55	69	238.3
	HLA-DPA1*01:03/DPB1*02:01	5.36	EVRSYCYLATVSDLS	55	69	353.5
	HLA-DPA1*01:03/DPB1*02:01	8.26	VRSYCYLATVSDLST	56	70	388.8
	HLA-DPA1*02:01/DPB1*01:01	12.7	AEVRSYCYLATVSDL	54	68	225
	HLA-DPA1*02:01/DPB1*01:01	3.34	EVRSYCYLATVSDLS	55	69	227.9
	HLA-DPA1*02:01/DPB1*01:01	3.32	RSYCYLATVSDLSTK	57	71	228.8
	HLA-DPA1*02:01/DPB1*01:01	3.42	VRSYCYLATVSDLST	56	70	230
	HLA-DPA1*01:03/DPB1*02:01	8.56	RSYCYLATVSDLSTK	57	71	479.3
	HLA-DPA1*01:03/DPB1*02:01	12.1	SYCYLATVSDLSTKA	58	72	752
	HLA-DPA1*01:03/DPB1*02:01	19.53	YCYLATVSDLSTKAA	59	73	952.8
	HLA-DPA1*02:01/DPB1*01:01	3.42	SYCYLATVSDLSTKA	58	72	287.8
	HLA-DPA1*02:01/DPB1*01:01	4.52	YCYLATVSDLSTKAA	59	73	417.7
FGGAFRSLF	HLA-DQA1*01:02/DQB1*06:02	40.63	VRSYCYLATVSDLST	56	70	620.8
	HLA-DQA1*01:02/DQB1*06:02	35.71	AEVRSYCYLATVSDL	54	68	627.3
	HLA-DQA1*01:02/DQB1*06:02	34.2	EVRSYCYLATVSDLS	55	69	648.6
	HLA-DPA1*02:01/DPB1*01:01	13.1	CYLATVSDLSTKAAC	60	74	618.8
	HLA-DQA1*01:02/DQB1*06:02	39.49	RSYCYLATVSDLSTK	57	71	806.7
	HLA-DRB5*01:01	2.58	KAVHQVFEGGAFRSLF	440	454	13.5
	HLA-DRB5*01:01	2.91	AVHQVFEGGAFRSLFG	441	455	18.2
	HLA-DRB1*08:02	3.52	QVFEGGAFRSLFGGMS	444	458	356.1
	HLA-DRB1*08:02	4.16	VFGGAFRSLFGGMSW	445	459	369.3
	HLA-DRB5*01:01	4.34	VHQVFEGGAFRSLFGG	442	456	23.2
	HLA-DPA1*01/DPB1*04:01	0.93	KAVHQVFEGGAFRSLF	440	454	361.4
	HLA-DPA1*01/DPB1*04:01	0.97	AVHQVFEGGAFRSLFG	441	455	452.4
	HLA-DPA1*01/DPB1*04:01	1.03	VHQVFEGGAFRSLFGG	442	456	526.5
	HLA-DPA1*01/DPB1*04:01	0.99	HQVFEGGAFRSLFGGM	443	457	434.4
	HLA-DPA1*01/DPB1*04:01	4.06	QVFEGGAFRSLFGGMS	444	458	443.3
	HLA-DPA1*01/DPB1*04:01	4.87	VFGGAFRSLFGGMSW	445	459	433.6
	HLA-DRB5*01:01	4.35	HQVFEGGAFRSLFGGM	443	457	27.3
	HLA-DRB1*03:01	1.25	KAVHQVFEGGAFRSLF	440	454	722.4
	HLA-DRB1*03:01	1.34	AVHQVFEGGAFRSLFG	441	455	680.6
	HLA-DRB1*03:01	1.42	VHQVFEGGAFRSLFGG	442	456	708.6
	HLA-DRB1*03:01	1.38	HQVFEGGAFRSLFGGM	443	457	505.6
	HLA-DRB1*11:01	1.28	HQVFEGGAFRSLFGGM	443	457	57.1
	HLA-DRB1*08:02	8.86	AVHQVFEGGAFRSLFG	441	455	825.7
	HLA-DRB1*08:02	11.55	VHQVFEGGAFRSLFGG	442	456	746.7

	HLA-DRB1*11:01	1.47	KAVHQVFEGGAFRSLF	440	454	268.5
	HLA-DRB1*11:01	1.41	AVHQVFEGGAFRSLFG	441	455	143.9
	HLA-DRB1*11:01	1.34	VHQVFEGGAFRSLFGG	442	456	94
	HLA-DRB1*08:02	13.97	HQVFEGGAFRSLFGGM	443	457	544.7
	HLA-DQA1*05:01/DQB1*02:01	36.57	AVHQVFEGGAFRSLFG	441	455	644.2
	HLA-DQA1*05:01/DQB1*02:01	39.48	KAVHQVFEGGAFRSLF	440	454	823.4
	HLA-DPA1*02:01/DPB1*01:01	0.08	VHQVFEGGAFRSLFGG	442	456	199.8
	HLA-DRB1*09:01	9.14	HQVFEGGAFRSLFGGM	443	457	310.5
	HLA-DRB1*04:05	9.78	KAVHQVFEGGAFRSLF	440	454	232.3
	HLA-DRB1*04:05	9	AVHQVFEGGAFRSLFG	441	455	251.9
	HLA-DRB1*04:05	9.07	VHQVFEGGAFRSLFGG	442	456	288.5
	HLA-DRB1*04:05	8.81	HQVFEGGAFRSLFGGM	443	457	294.1
	HLA-DQA1*05:01/DQB1*02:01	38.33	VHQVFEGGAFRSLFGG	442	456	934.3
	HLA-DRB1*09:01	8.48	VHQVFEGGAFRSLFGG	442	456	336.9
	HLA-DRB1*09:01	8.31	AVHQVFEGGAFRSLFG	441	455	354.3
	HLA-DPA1*02:01/DPB1*01:01	0.08	HQVFEGGAFRSLFGGM	443	457	246.9
	HLA-DRB1*09:01	5.92	KAVHQVFEGGAFRSLF	440	454	456.1
	HLA-DPA1*02:01/DPB1*01:01	0.51	QVFEGGAFRSLFGGMS	444	458	358.5
	HLA-DPA1*02:01/DPB1*01:01	0.55	VFGGAFRSLFGGMSW	445	459	466
	HLA-DPA1*02:01/DPB1*01:01	29.41	FGGAFRSLFGGMSWI	446	460	528.8
FLAVGGVLL	HLA-DRB1*01:01	0.14	RSIALTFLAVGGVLL	479	493	7.9
	HLA-DRB1*01:01	0.14	IALTFLAVGGVLLFL	481	495	7.8
	HLA-DRB1*01:01	0.14	ALTFLAVGGVLLFLS	482	496	9.3
	HLA-DRB1*01:01	0.14	LTFLAVGGVLLFLSV	483	497	14
	HLA-DRB1*01:01	1.15	TFLAVGGVLLFLSVN	484	498	23.9
	HLA-DRB1*01:01	1.15	FLAVGGVLLFLSVNV	485	499	30.1
	HLA-DRB1*04:05	2.29	FLAVGGVLLFLSVNV	485	499	309.1
	HLA-DPA1*01/DPB1*04:01	0.79	RSIALTFLAVGGVLL	479	493	275.5
	HLA-DPA1*01/DPB1*04:01	1.87	FLAVGGVLLFLSVNV	485	499	804.1
	HLA-DPA1*01:03/DPB1*02:01	0.37	RSIALTFLAVGGVLL	479	493	386.6
	HLA-DPA1*01/DPB1*04:01	1.68	IALTFLAVGGVLLFL	481	495	340
	HLA-DPA1*01/DPB1*04:01	1.65	ALTFLAVGGVLLFLS	482	496	369.5
	HLA-DPA1*01/DPB1*04:01	0.78	LTFLAVGGVLLFLSV	483	497	374.7
	HLA-DPA1*01/DPB1*04:01	1.88	TFLAVGGVLLFLSVN	484	498	437.5
	HLA-DPA1*01/DPB1*04:01	0.97	SIALTFLAVGGVLLF	480	494	330.1
	HLA-DPA1*03:01/DPB1*04:02	0.13	SIALTFLAVGGVLLF	480	494	142.4
	HLA-DPA1*03:01/DPB1*04:02	0.09	IALTFLAVGGVLLFL	481	495	103.9
	HLA-DPA1*03:01/DPB1*04:02	0.09	ALTFLAVGGVLLFLS	482	496	73.3
	HLA-DPA1*03:01/DPB1*04:02	0.08	LTFLAVGGVLLFLSV	483	497	80
	HLA-DPA1*03:01/DPB1*04:02	0.26	TFLAVGGVLLFLSVN	484	498	97.6
	HLA-DPA1*03:01/DPB1*04:02	0.32	FLAVGGVLLFLSVNV	485	499	119.5
	HLA-DQA1*05:01/DQB1*02:01	6.19	LTFLAVGGVLLFLSV	483	497	907.7
	HLA-DQA1*05:01/DQB1*03:01	17.33	IALTFLAVGGVLLFL	481	495	39.4
	HLA-DRB1*07:01	0.14	ALTFLAVGGVLLFLS	482	496	301.2
	HLA-DRB1*07:01	0.14	LTFLAVGGVLLFLSV	483	497	465.3
	HLA-DRB1*07:01	0.59	TFLAVGGVLLFLSVN	484	498	835.8
	HLA-DRB1*15:01	10.47	TFLAVGGVLLFLSVN	484	498	303.1
	HLA-DRB1*04:05	9.23	RSIALTFLAVGGVLL	479	493	617.9
	HLA-DRB1*04:05	9.48	SIALTFLAVGGVLLF	480	494	697.5
	HLA-DRB1*04:05	8.99	IALTFLAVGGVLLFL	481	495	641.4
	HLA-DRB1*04:05	6.4	ALTFLAVGGVLLFLS	482	496	525.6
	HLA-DRB1*04:05	6.44	LTFLAVGGVLLFLSV	483	497	590.4
	HLA-DPA1*01:03/DPB1*02:01	0.41	SIALTFLAVGGVLLF	480	494	460.4
	HLA-DRB1*04:05	8.78	TFLAVGGVLLFLSVN	484	498	483.4
	HLA-DPA1*02:01/DPB1*01:01	0.52	ALTFLAVGGVLLFLS	482	496	130.6
	HLA-DPA1*02:01/DPB1*01:01	0.48	LTFLAVGGVLLFLSV	483	497	136.8
	HLA-DRB3*01:01	0.47	ALTFLAVGGVLLFLS	482	496	671.1
	HLA-DRB3*01:01	0.47	IALTFLAVGGVLLFL	481	495	703.9
	HLA-DQA1*05:01/DQB1*03:01	19.26	RSIALTFLAVGGVLL	479	493	96.1
	HLA-DPA1*01:03/DPB1*02:01	0.63	ALTFLAVGGVLLFLS	482	496	251
	HLA-DPA1*02:01/DPB1*01:01	0.83	RSIALTFLAVGGVLL	479	493	332.7
	HLA-DPA1*01:03/DPB1*02:01	0.75	IALTFLAVGGVLLFL	481	495	255.2
	HLA-DPA1*02:01/DPB1*01:01	0.84	TFLAVGGVLLFLSVN	484	498	162.5
	HLA-DPA1*02:01/DPB1*01:01	0.87	SIALTFLAVGGVLLF	480	494	398.7
	HLA-DPA1*02:01/DPB1*01:01	1.03	IALTFLAVGGVLLFL	481	495	216.8
FLVHREWF M	HLA-DRB1*07:01	4.04	TVGKTFLVHREWFMD	205	219	6.8
	HLA-DPA1*01:03/DPB1*02:01	4.32	TVGKTFLVHREWFMD	205	219	124.6
	HLA-DPA1*01/DPB1*04:01	5.27	VGKTFLVHREWFMD	206	220	168.9
	HLA-DPA1*01/DPB1*04:01	5.38	TVGKTFLVHREWFMD	205	219	184.5
	HLA-DPA1*01:03/DPB1*02:01	2.42	VGKTFLVHREWFMD	206	220	86.3

	HLA-DPA1*02:01/DPB1*05:01	14.71	KTFLVHREWFMDLNL	209	223	403.2
	HLA-DRB1*07:01	8.98	GTKTFLVHREWFMDL	207	221	10.2
	HLA-DRB1*07:01	9	KTFLVHREWFMDLNL	209	223	20.6
	HLA-DQA1*05:01/DQB1*02:01	42.27	TVGKTFLVHREWFMDL	205	219	402.5
	HLA-DRB1*07:01	9.09	TKTFLVHREWFMDLN	208	222	16.2
	HLA-DRB1*07:01	9.71	VGKTFLVHREWFMD	206	220	9.4
	HLA-DRB1*15:01	12.66	KTFLVHREWFMDLNL	209	223	102.1
	HLA-DRB1*03:01	1.59	TKTFLVHREWFMDLN	208	222	381.8
	HLA-DRB1*15:01	12.64	TKTFLVHREWFMDLN	208	222	126.1
	HLA-DRB1*15:01	25.84	TFLVHREWFMDLNL	210	224	127
	HLA-DRB1*15:01	9.92	TVGKTFLVHREWFMD	205	219	191.9
	HLA-DRB1*15:01	12.29	GTKTFLVHREWFMDL	207	221	132.4
	HLA-DRB1*15:01	12.64	VGKTFLVHREWFMD	206	220	176
	HLA-DRB1*03:01	1.59	KTFLVHREWFMDLNL	209	223	431
	HLA-DQA1*01:01/DQB1*05:01	13.57	GTKTFLVHREWFMDL	207	221	542.2
	HLA-DRB1*03:01	1.59	GTKTFLVHREWFMDL	207	221	482.3
	HLA-DRB5*01:01	8.41	TKTFLVHREWFMDLN	208	222	115.7
	HLA-DRB1*07:01	16.87	FLVHREWFMDLNL	211	225	45.1
	HLA-DRB1*04:01	17.2	TVGKTFLVHREWFMD	205	219	861.6
	HLA-DRB1*07:01	18.15	TFLVHREWFMDLNL	210	224	34.2
	HLA-DRB5*01:01	8.36	GTKTFLVHREWFMDL	207	221	141.4
	HLA-DRB5*01:01	8.51	KTFLVHREWFMDLNL	209	223	145
	HLA-DRB5*01:01	16.56	FLVHREWFMDLNL	211	225	412.9
	HLA-DRB1*04:01	18.46	KTFLVHREWFMDLNL	209	223	605.7
	HLA-DRB5*01:01	18.53	TFLVHREWFMDLNL	210	224	281.8
	HLA-DRB1*04:01	18.56	GTKTFLVHREWFMDL	207	221	658
	HLA-DRB1*04:01	18.61	TKTFLVHREWFMDLN	208	222	484.1
	HLA-DRB1*04:01	18.68	VGKTFLVHREWFMD	206	220	829.6
	HLA-DQA1*01:01/DQB1*05:01	21.16	VGKTFLVHREWFMD	206	220	919.7
	HLA-DRB5*01:01	8.97	TVGKTFLVHREWFMD	205	219	293.8
	HLA-DRB5*01:01	9.02	VGKTFLVHREWFMD	206	220	254.5
	HLA-DQA1*05:01/DQB1*02:01	23.77	TFLVHREWFMDLNL	210	224	212.8
	HLA-DQA1*05:01/DQB1*02:01	29.34	KTFLVHREWFMDLNL	209	223	209.4
	HLA-DRB1*04:01	34.13	TFLVHREWFMDLNL	210	224	668.5
	HLA-DQA1*05:01/DQB1*02:01	34.31	GTKTFLVHREWFMDL	207	221	218.2
	HLA-DQA1*05:01/DQB1*02:01	36.35	TKTFLVHREWFMDLN	208	222	212.7
	HLA-DQA1*05:01/DQB1*02:01	38.76	VGKTFLVHREWFMD	206	220	281
	HLA-DRB1*01:01	47.6	TVGKTFLVHREWFMD	205	219	147
	HLA-DRB1*01:01	49.19	GTKTFLVHREWFMDL	207	221	109.9
	HLA-DRB1*01:01	50.22	TKTFLVHREWFMDLN	208	222	95.8
	HLA-DRB1*01:01	50.34	KTFLVHREWFMDLNL	209	223	135.8
	HLA-DRB1*01:01	50.47	VGKTFLVHREWFMD	206	220	160.9
	HLA-DRB1*01:01	64.34	TFLVHREWFMDLNL	210	224	212.6
	HLA-DRB1*01:01	62.78	FLVHREWFMDLNL	211	225	301.6
FRSLFGGMS	HLA-DRB5*01:01	0.28	GGAFRSLFGGMSWIT	447	461	3.1
	HLA-DRB5*01:01	0.29	GAFRSLFGGMSWITQ	448	462	3.6
	HLA-DRB5*01:01	0.28	FGGAFRSLFGGMSWI	446	460	3.7
	HLA-DRB1*11:01	0.09	QVFGGAFRSLFGGMS	444	458	25.3
	HLA-DRB1*11:01	0.1	VFGGAFRSLFGGMSW	445	459	21.7
	HLA-DRB1*11:01	0.09	FGGAFRSLFGGMSWI	446	460	16
	HLA-DRB1*11:01	0.09	GGAFRSLFGGMSWIT	447	461	10.8
	HLA-DRB1*11:01	0.09	GAFRSLFGGMSWITQ	448	462	14.5
	HLA-DRB1*11:01	0.56	AFRSLFGGMSWITQG	449	463	21
	HLA-DRB1*11:01	0.57	FRSLFGGMSWITQGL	450	464	32.9
	HLA-DRB5*01:01	0.28	QVFGGAFRSLFGGMS	444	458	7.3
	HLA-DRB5*01:01	0.3	VFGGAFRSLFGGMSW	445	459	5.3
	HLA-DRB5*01:01	1.23	AFRSLFGGMSWITQG	449	463	4.6
	HLA-DRB5*01:01	1.27	FRSLFGGMSWITQGL	450	464	6.2
	HLA-DRB1*01:01	2.05	GGAFRSLFGGMSWIT	447	461	4.3
	HLA-DRB1*01:01	2.27	FGGAFRSLFGGMSWI	446	460	4.8
	HLA-DRB1*01:01	2.27	GAFRSLFGGMSWITQ	448	462	4.6
	HLA-DRB1*01:01	2.51	VFGGAFRSLFGGMSW	445	459	6.2
	HLA-DRB1*04:05	2.81	GAFRSLFGGMSWITQ	448	462	55.2
	HLA-DRB1*08:02	4.12	GGAFRSLFGGMSWIT	447	461	895.2
	HLA-DRB1*08:02	4.13	FGGAFRSLFGGMSWI	446	460	525.7
	HLA-DRB1*04:05	3.52	FGGAFRSLFGGMSWI	446	460	44.4
	HLA-DRB1*04:05	3.49	GGAFRSLFGGMSWIT	447	461	44.7
	HLA-DRB1*04:01	1.59	GAFRSLFGGMSWITQ	448	462	78.7
	HLA-DRB1*04:01	2.33	AFRSLFGGMSWITQG	449	463	94.5
	HLA-DRB1*04:01	2.26	FRSLFGGMSWITQGL	450	464	139.1
	HLA-DRB1*04:01	3.84	QVFGGAFRSLFGGMS	444	458	218.8

	HLA-DRB1*04:01	4.23	VFGGAFRSLFGGMSW	445	459	186.4
	HLA-DRB1*04:01	4.26	FGGAFRSLFGGMSWI	446	460	144.4
	HLA-DRB1*04:01	3.64	GGAFRSLFGGMSWIT	447	461	125.7
	HLA-DRB1*04:05	3.64	VFGGAFRSLFGGMSW	445	459	46.7
	HLA-DRB1*01:01	2.27	QVFGGAFRSLFGGMS	444	458	9.4
	HLA-DRB1*04:05	2.97	QVFGGAFRSLFGGMS	444	458	50.9
	HLA-DRB1*04:05	5.51	FRSLFGGMSWITQGL	450	464	117.3
	HLA-DRB1*04:05	5.57	AFRSLFGGMSWITQG	449	463	74.1
	HLA-DRB1*09:01	0.16	QVFGGAFRSLFGGMS	444	458	103
	HLA-DRB1*09:01	0.17	VFGGAFRSLFGGMSW	445	459	111.6
	HLA-DRB1*01:01	8.28	AFRSLFGGMSWITQG	449	463	5.1
	HLA-DRB1*01:01	8.28	FRSLFGGMSWITQGL	450	464	6
	HLA-DRB1*09:01	0.15	GGAFRSLFGGMSWIT	447	461	124.3
	HLA-DRB1*09:01	0.16	GAFRSLFGGMSWITQ	448	462	124.5
	HLA-DRB1*09:01	0.16	FGGAFRSLFGGMSWI	446	460	127.1
	HLA-DRB1*09:01	1.57	AFRSLFGGMSWITQG	449	463	164.2
	HLA-DRB1*09:01	1.6	FRSLFGGMSWITQGL	450	464	203.4
	HLA-DQA1*05:01/DQB1*03:01	23.94	QVFGGAFRSLFGGMS	444	458	40.4
	HLA-DQA1*05:01/DQB1*03:01	27.86	VFGGAFRSLFGGMSW	445	459	49.9
	HLA-DRB1*07:01	5.3	QVFGGAFRSLFGGMS	444	458	697.5
	HLA-DRB1*07:01	6.48	VFGGAFRSLFGGMSW	445	459	773.8
	HLA-DQA1*05:01/DQB1*03:01	30.55	FGGAFRSLFGGMSWI	446	460	63.4
	HLA-DRB1*07:01	6.03	FGGAFRSLFGGMSWI	446	460	536.8
FSSNTVKLT	HLA-DRB1*04:01	3.26	GAIPVEFSSNTVKLT	268	282	168.4
	HLA-DRB1*04:01	3.39	AIPVEFSSNTVKLTS	269	283	101.9
	HLA-DRB1*04:01	4.36	IPVEFSSNTVKLTSG	270	284	74.7
	HLA-DRB1*04:01	4.6	PVEFSSNTVKLTSGH	271	285	63.7
	HLA-DRB1*04:01	5.72	VEFSSNTVKLTSGHL	272	286	96.8
	HLA-DRB3*01:01	0.11	AIPVEFSSNTVKLTS	269	283	187.5
	HLA-DRB3*01:01	0.11	GAIPVEFSSNTVKLT	268	282	195.3
	HLA-DRB3*01:01	0.12	IPVEFSSNTVKLTSG	270	284	211.5
	HLA-DRB3*01:01	0.12	PVEFSSNTVKLTSGH	271	285	229.8
	HLA-DRB1*11:01	1.82	GAIPVEFSSNTVKLT	268	282	419.1
	HLA-DRB1*11:01	1.57	AIPVEFSSNTVKLTS	269	283	197.3
	HLA-DRB1*11:01	1.52	IPVEFSSNTVKLTSG	270	284	115.5
	HLA-DRB1*11:01	1.6	PVEFSSNTVKLTSGH	271	285	64.8
	HLA-DRB1*11:01	1.06	VEFSSNTVKLTSGHL	272	286	111
	HLA-DRB1*11:01	1.5	EFSSNTVKLTSGHLK	273	287	195.1
	HLA-DRB1*11:01	1.61	FSSNTVKLTSGHLKC	274	288	311
	HLA-DRB3*01:01	0.12	VEFSSNTVKLTSGHL	272	286	500.6
	HLA-DRB1*04:01	12.6	EFSSNTVKLTSGHLK	273	287	153.8
	HLA-DRB1*04:05	12.12	AIPVEFSSNTVKLTS	269	283	569.2
	HLA-DRB1*04:05	12.19	GAIPVEFSSNTVKLT	268	282	663
	HLA-DRB1*04:01	13.65	FSSNTVKLTSGHLKC	274	288	393.7
	HLA-DRB1*04:05	13.8	IPVEFSSNTVKLTSG	270	284	601.3
	HLA-DRB1*04:05	13.86	VEFSSNTVKLTSGHL	272	286	867.3
	HLA-DRB1*04:05	14.06	PVEFSSNTVKLTSGH	271	285	617.3
	HLA-DPA1*03:01/DPB1*04:02	6.29	PVEFSSNTVKLTSGH	271	285	184
	HLA-DRB1*01:01	15.82	VEFSSNTVKLTSGHL	272	286	63.5
	HLA-DPA1*03:01/DPB1*04:02	7.79	VEFSSNTVKLTSGHL	272	286	244.5
	HLA-DRB1*01:01	21.8	PVEFSSNTVKLTSGH	271	285	59.5
	HLA-DPA1*02:01/DPB1*01:01	4.32	GAIPVEFSSNTVKLT	268	282	611.4
	HLA-DPA1*02:01/DPB1*01:01	4.1	AIPVEFSSNTVKLTS	269	283	490.7
	HLA-DPA1*02:01/DPB1*01:01	4.22	IPVEFSSNTVKLTSG	270	284	495.2
	HLA-DPA1*02:01/DPB1*01:01	4.33	PVEFSSNTVKLTSGH	271	285	598.1
	HLA-DRB1*09:01	7.77	PVEFSSNTVKLTSGH	271	285	627.4
	HLA-DRB1*01:01	21.44	IPVEFSSNTVKLTSG	270	284	119
	HLA-DRB1*09:01	7.7	IPVEFSSNTVKLTSG	270	284	762.9
	HLA-DQA1*05:01/DQB1*03:01	33.91	GAIPVEFSSNTVKLT	268	282	441.6
	HLA-DQA1*05:01/DQB1*03:01	33.86	AIPVEFSSNTVKLTS	269	283	549.2
	HLA-DQA1*05:01/DQB1*03:01	34.15	IPVEFSSNTVKLTSG	270	284	535.1
	HLA-DQA1*05:01/DQB1*03:01	35.14	PVEFSSNTVKLTSGH	271	285	567.3
	HLA-DRB1*09:01	6.44	AIPVEFSSNTVKLTS	269	283	855.2
	HLA-DQA1*05:01/DQB1*03:01	35.86	VEFSSNTVKLTSGHL	272	286	648.9
	HLA-DPA1*02:01/DPB1*01:01	6.22	VEFSSNTVKLTSGHL	272	286	720.2
	HLA-DRB1*01:01	18.99	AIPVEFSSNTVKLTS	269	283	190.7
	HLA-DQA1*05:01/DQB1*03:01	41.45	EFSSNTVKLTSGHLK	273	287	734.6
	HLA-DQA1*05:01/DQB1*03:01	41.95	FSSNTVKLTSGHLKC	274	288	781.9
FVSVATANA	HLA-DRB1*08:02	0.07	VNPFVSVATANAKVL	358	372	28.2
	HLA-DRB1*08:02	0.07	NPFVSVATANAKVLI	359	373	30
	HLA-DRB1*08:02	0.07	TVNPFVSVATANAKV	357	371	33.5

	HLA-DRB1*04:01	0.2	VNPFVSVATANAKVL	358	372	9.5
	HLA-DRB1*04:01	0.22	TVNPFVSVATANAKV	357	371	10.4
	HLA-DRB1*08:02	0.07	VTNPFVSVATANAK	356	370	37.6
	HLA-DRB1*08:02	0.08	LVTNPFVSVATANA	355	369	47.5
	HLA-DRB1*08:02	0.33	PFVSVATANAKVLIE	360	374	39.6
	HLA-DRB1*04:01	0.23	VTNPFVSVATANAK	356	370	12.2
	HLA-DRB1*08:02	0.37	FVSVATANAKVLIEL	361	375	107
	HLA-DRB1*04:01	0.22	NPFVSVATANAKVLI	359	373	13.6
	HLA-DRB1*04:01	0.24	LVTNPFVSVATANA	355	369	16.4
	HLA-DRB1*09:01	0.7	LVTNPFVSVATANA	355	369	22.2
	HLA-DRB1*09:01	0.7	VTNPFVSVATANAK	356	370	16.3
	HLA-DRB1*11:01	0.7	VNPFVSVATANAKVL	358	372	58
	HLA-DRB1*11:01	0.73	NPFVSVATANAKVLI	359	373	103.4
	HLA-DRB1*09:01	0.79	VNPFVSVATANAKVL	358	372	10.5
	HLA-DRB1*09:01	0.81	NPFVSVATANAKVLI	359	373	15.3
	HLA-DRB1*11:01	0.84	TVNPFVSVATANAKV	357	371	120.1
	HLA-DRB1*11:01	0.91	VTNPFVSVATANAK	356	370	269.9
	HLA-DRB1*11:01	0.94	LVTNPFVSVATANA	355	369	722.9
	HLA-DRB1*04:01	0.96	PFVSVATANAKVLIE	360	374	22.1
	HLA-DRB1*04:01	0.96	FVSVATANAKVLIEL	361	375	67.3
	HLA-DRB1*04:05	1.41	VNPFVSVATANAKVL	358	372	17.4
	HLA-DRB1*09:01	1.02	TVNPFVSVATANAKV	357	371	12.4
	HLA-DRB1*04:05	1.51	TVNPFVSVATANAKV	357	371	19.7
	HLA-DRB1*04:05	1.46	NPFVSVATANAKVLI	359	373	22.5
	HLA-DRB1*04:05	1.61	VTNPFVSVATANAK	356	370	23.2
	HLA-DRB1*04:05	1.62	LVTNPFVSVATANA	355	369	29.9
	HLA-DRB1*01:01	2.05	VNPFVSVATANAKVL	358	372	5.5
	HLA-DRB1*09:01	2.37	PFVSVATANAKVLIE	360	374	26.8
	HLA-DRB1*11:01	2.55	FVSVATANAKVLIEL	361	375	421.2
	HLA-DRB1*01:01	2.27	NPFVSVATANAKVLI	359	373	6.9
	HLA-DRB1*07:01	0.96	VNPFVSVATANAKVL	358	372	14.2
	HLA-DRB1*11:01	2.65	PFVSVATANAKVLIE	360	374	208.4
	HLA-DRB1*04:05	4.81	PFVSVATANAKVLIE	360	374	33.7
	HLA-DRB1*07:01	1.63	LVTNPFVSVATANA	355	369	33
	HLA-DRB1*07:01	1.69	VTNPFVSVATANAK	356	370	35.7
	HLA-DRB1*07:01	1.25	TVNPFVSVATANAKV	357	371	19.7
	HLA-DRB1*07:01	0.94	NPFVSVATANAKVLI	359	373	17.4
	HLA-DRB1*07:01	1.48	PFVSVATANAKVLIE	360	374	26
	HLA-DRB1*09:01	2.35	FVSVATANAKVLIEL	361	375	56.1
	HLA-DRB1*01:01	2.51	TVNPFVSVATANAKV	357	371	8.5
	HLA-DRB1*04:05	4.93	FVSVATANAKVLIEL	361	375	62.4
	HLA-DRB1*03:01	4.69	VNPFVSVATANAKVL	358	372	477.6
	HLA-DRB1*01:01	3.02	LVTNPFVSVATANA	355	369	30.5
	HLA-DRB1*01:01	2.74	VTNPFVSVATANAK	356	370	15.9
	HLA-DRB1*01:01	6.87	PFVSVATANAKVLIE	360	374	8.2
	HLA-DRB1*01:01	6.65	FVSVATANAKVLIEL	361	375	8.7
	HLA-DRB1*13:02	25.36	VTNPFVSVATANAK	356	370	189.3
	HLA-DRB1*15:01	15.76	NPFVSVATANAKVLI	359	373	408.8
	HLA-DRB1*15:01	21.44	FVSVATANAKVLIEL	361	375	832.2
	HLA-DRB1*15:01	21.98	PFVSVATANAKVLIE	360	374	488.7
IKYEVAIFV	HLA-DRB1*09:01	1.51	TILKENIKYEVAIFV	129	143	524.1
	HLA-DRB1*09:01	1.71	ILKENIKYEVAIFVH	130	144	607.2
	HLA-DPA1*02:01/DPB1*05:01	2.48	KENIKYEVAIFVHGP	132	146	145.9
	HLA-DPA1*02:01/DPB1*05:01	2.64	ENIKYEVAIFVHGPT	133	147	148.4
	HLA-DRB1*15:01	2.73	ENIKYEVAIFVHGPT	133	147	17.6
	HLA-DRB1*15:01	4.75	NIKYEVAIFVHGPTT	134	148	20
	HLA-DRB1*15:01	3.91	IKYEVAIFVHGPTTV	135	149	30.5
	HLA-DRB1*15:01	4	TILKENIKYEVAIFV	129	143	20.4
	HLA-DRB1*15:01	4.14	ILKENIKYEVAIFVH	130	144	16.5
	HLA-DRB1*15:01	4.41	LKENIKYEVAIFVHG	131	145	16.2
	HLA-DRB1*15:01	4.72	KENIKYEVAIFVHGP	132	146	16
	HLA-DRB1*03:01	1.23	ILKENIKYEVAIFVH	130	144	70.9
	HLA-DRB1*04:01	4.43	LKENIKYEVAIFVHG	131	145	160.8
	HLA-DPA1*02:01/DPB1*05:01	5.91	NIKYEVAIFVHGPTT	134	148	202
	HLA-DRB1*04:01	4.52	KENIKYEVAIFVHGP	132	146	132.3
	HLA-DRB1*04:01	4.92	TILKENIKYEVAIFV	129	143	317.8
	HLA-DRB1*04:01	4.93	ILKENIKYEVAIFVH	130	144	266.3
	HLA-DRB1*04:01	4.98	ENIKYEVAIFVHGPT	133	147	169.7
	HLA-DRB1*03:01	1.15	TILKENIKYEVAIFV	129	143	107.3
	HLA-DRB1*03:01	1.4	KENIKYEVAIFVHGP	132	146	109.4
	HLA-DRB1*03:01	1.32	LKENIKYEVAIFVHG	131	145	110.1

	HLA-DRB1*07:01	1.01	TILKENIKYEVAIFV	129	143	36.6
	HLA-DRB1*07:01	1.01	ILKENIKYEVAIFVH	130	144	43.8
	HLA-DRB1*04:01	8.21	IKYEVAIFVHGPTTV	135	149	326.8
	HLA-DRB1*03:01	1.42	ENIKYEVAIFVHGPT	133	147	228.2
	HLA-DRB1*03:01	5.62	NIKYEVAIFVHGPTT	134	148	577.1
	HLA-DRB5*01:01	0.78	LKENIKYEVAIFVHG	131	145	47.5
	HLA-DRB5*01:01	0.84	KENIKYEVAIFVHGP	132	146	47.6
	HLA-DRB5*01:01	0.75	TILKENIKYEVAIFV	129	143	112
	HLA-DRB5*01:01	0.74	ILKENIKYEVAIFVH	130	144	65.4
	HLA-DRB5*01:01	0.87	ENIKYEVAIFVHGPT	133	147	88.7
	HLA-DRB5*01:01	2.93	NIKYEVAIFVHGPTT	134	148	138.3
	HLA-DRB5*01:01	2.97	IKYEVAIFVHGPTTV	135	149	261.4
	HLA-DRB1*13:02	5.27	LKENIKYEVAIFVHG	131	145	218.2
	HLA-DPA1*01:03/DPB1*02:01	1.33	TILKENIKYEVAIFV	129	143	316.1
	HLA-DPA1*01:03/DPB1*02:01	1.27	ILKENIKYEVAIFVH	130	144	225.8
	HLA-DPA1*01:03/DPB1*02:01	0.7	LKENIKYEVAIFVHG	131	145	218.1
	HLA-DPA1*01:03/DPB1*02:01	0.71	KENIKYEVAIFVHGP	132	146	207.3
	HLA-DPA1*01:03/DPB1*02:01	0.73	ENIKYEVAIFVHGPT	133	147	223.9
	HLA-DPA1*01:03/DPB1*02:01	1.43	NIKYEVAIFVHGPTT	134	148	279.9
	HLA-DPA1*01:03/DPB1*02:01	1.49	IKYEVAIFVHGPTTV	135	149	316.4
	HLA-DRB3*01:01	0.02	TILKENIKYEVAIFV	129	143	410.3
	HLA-DRB1*04:01	10.84	NIKYEVAIFVHGPTT	134	148	205.7
	HLA-DRB3*01:01	0.02	ILKENIKYEVAIFVH	130	144	456.2
	HLA-DRB1*07:01	1.08	LKENIKYEVAIFVHG	131	145	76.9
	HLA-DRB1*11:01	2.19	LKENIKYEVAIFVHG	131	145	544.1
	HLA-DRB1*11:01	2.92	KENIKYEVAIFVHGP	132	146	562.4
	HLA-DRB3*01:01	0.02	LKENIKYEVAIFVHG	131	145	555.1
	HLA-DPA1*02:01/DPB1*01:01	0.41	KENIKYEVAIFVHGP	132	146	131.1
	HLA-DRB1*04:05	10.45	LKENIKYEVAIFVHG	131	145	842.8
	HLA-DRB1*04:05	10.88	KENIKYEVAIFVHGP	132	146	950.9
	HLA-DRB3*01:01	0.02	KENIKYEVAIFVHGP	132	146	648.5
	HLA-DPA1*02:01/DPB1*01:01	0.45	ILKENIKYEVAIFVH	130	144	143.4
	HLA-DPA1*02:01/DPB1*01:01	0.33	LKENIKYEVAIFVHG	131	145	145.9
	HLA-DRB1*04:05	10.42	TILKENIKYEVAIFV	129	143	834.7
	HLA-DRB1*04:05	10.47	ILKENIKYEVAIFVH	130	144	739.9
	HLA-DPA1*02:01/DPB1*01:01	0.43	ENIKYEVAIFVHGPT	133	147	152
	HLA-DRB1*07:01	1.13	KENIKYEVAIFVHGP	132	146	123.7
	HLA-DRB1*13:02	5.59	KENIKYEVAIFVHGP	132	146	542.4
	HLA-DRB1*13:02	5.65	ENIKYEVAIFVHGPT	133	147	703
	HLA-DRB1*13:02	14.22	NIKYEVAIFVHGPTT	134	148	882.1
	HLA-DPA1*02:01/DPB1*01:01	1.49	NIKYEVAIFVHGPTT	134	148	188.3
	HLA-DPA1*01/DPB1*04:01	4.39	KENIKYEVAIFVHGP	132	146	651.8
	HLA-DPA1*01/DPB1*04:01	4.35	LKENIKYEVAIFVHG	131	145	653.9
	HLA-DPA1*02:01/DPB1*01:01	0.3	TILKENIKYEVAIFV	129	143	277.2
	HLA-DPA1*01/DPB1*04:01	5.22	IKYEVAIFVHGPTTV	135	149	688.1
	HLA-DPA1*01/DPB1*04:01	4.42	ENIKYEVAIFVHGPT	133	147	704.5
	HLA-DRB1*01:01	18.22	LKENIKYEVAIFVHG	131	145	29.5
	HLA-DPA1*01/DPB1*04:01	5.16	NIKYEVAIFVHGPTT	134	148	735.3
	HLA-DRB1*09:01	6.73	NIKYEVAIFVHGPTT	134	148	321.1
	HLA-DRB1*01:01	17.28	ILKENIKYEVAIFVH	130	144	40.6
	HLA-DRB1*01:01	18.99	KENIKYEVAIFVHGP	132	146	36.3
	HLA-DPA1*02:01/DPB1*01:01	1.39	IKYEVAIFVHGPTTV	135	149	240.2
	HLA-DRB1*09:01	1.91	ENIKYEVAIFVHGPT	133	147	372.8
	HLA-DPA1*01/DPB1*04:01	22.36	ILKENIKYEVAIFVH	130	144	822.6
	HLA-DRB1*07:01	1.2	ENIKYEVAIFVHGPT	133	147	198.7
	HLA-DRB1*04:05	22.35	NIKYEVAIFVHGPTT	134	148	995.7
	HLA-DRB4*01:01	6.49	ENIKYEVAIFVHGPT	133	147	403.6
	HLA-DRB1*09:01	1.74	LKENIKYEVAIFVHG	131	145	484.8
	HLA-DRB1*01:01	16.98	TILKENIKYEVAIFV	129	143	68
	HLA-DRB1*09:01	1.85	KENIKYEVAIFVHGP	132	146	533.4
	HLA-DQA1*05:01/DQB1*03:01	30.77	ENIKYEVAIFVHGPT	133	147	226.5
	HLA-DQA1*05:01/DQB1*03:01	31.7	NIKYEVAIFVHGPTT	134	148	177.4
	HLA-DRB1*01:01	19.51	ENIKYEVAIFVHGPT	133	147	87.6
	HLA-DQA1*05:01/DQB1*03:01	31.74	KENIKYEVAIFVHGP	132	146	442.5
	HLA-DQA1*05:01/DQB1*03:01	36.21	ILKENIKYEVAIFVH	130	144	430.6
	HLA-DQA1*05:01/DQB1*03:01	33.68	LKENIKYEVAIFVHG	131	145	435.4
	HLA-DQA1*05:01/DQB1*03:01	36.81	TILKENIKYEVAIFV	129	143	503.2
	HLA-DRB1*01:01	28.42	NIKYEVAIFVHGPTT	134	148	153.5
	HLA-DRB4*01:01	15.42	NIKYEVAIFVHGPTT	134	148	882
ITPAAPSYT	HLA-DRB1*09:01	0.64	AGRLSITPAAPSYTL	164	178	46.1
	HLA-DRB1*09:01	0.64	GRLSITPAAPSYTLK	165	179	37

	HLA-DRB1*09:01	0.67	QAGRLSITPAAPSYT	163	177	64.1
	HLA-DRB1*09:01	1.03	RLSITPAAPSYTLKL	166	180	31.8
	HLA-DRB1*09:01	1.08	LSITPAAPSYTLKLG	167	181	55.1
	HLA-DRB1*09:01	4.59	SITPAAPSYTLKLGE	168	182	95.9
	HLA-DRB1*09:01	4.64	ITPAAPSYTLKLGEY	169	183	183.3
	HLA-DRB1*01:01	19.37	RLSITPAAPSYTLKL	166	180	10.6
	HLA-DRB5*01:01	8.04	RLSITPAAPSYTLKL	166	180	286.3
	HLA-DRB5*01:01	8.45	LSITPAAPSYTLKLG	167	181	640.6
	HLA-DRB1*13:02	23.2	AGRLSITPAAPSYTL	164	178	455.3
	HLA-DRB1*13:02	23.23	GRLSITPAAPSYTLK	165	179	481.5
	HLA-DRB1*15:01	14.14	GRLSITPAAPSYTLK	165	179	436.4
	HLA-DQA1*05:01/DQB1*03:01	17.41	AGRLSITPAAPSYTL	164	178	16.5
	HLA-DRB1*13:02	25.68	RLSITPAAPSYTLKL	166	180	503.3
	HLA-DQA1*05:01/DQB1*03:01	17.71	GRLSITPAAPSYTLK	165	179	14.7
	HLA-DQA1*05:01/DQB1*03:01	18.42	QAGRLSITPAAPSYT	163	177	18.9
	HLA-DQA1*05:01/DQB1*03:01	18.89	RLSITPAAPSYTLKL	166	180	13.8
	HLA-DRB1*13:02	23.44	QAGRLSITPAAPSYT	163	177	604.3
	HLA-DQA1*05:01/DQB1*03:01	19.62	LSITPAAPSYTLKLG	167	181	13.7
	HLA-DRB1*15:01	21.13	RLSITPAAPSYTLKL	166	180	276.7
	HLA-DRB1*01:01	21.05	LSITPAAPSYTLKLG	167	181	21.4
	HLA-DRB1*15:01	21.52	LSITPAAPSYTLKLG	167	181	395.1
	HLA-DQA1*05:01/DQB1*03:01	23.91	SITPAAPSYTLKLGE	168	182	25.9
	HLA-DRB1*13:02	27.37	LSITPAAPSYTLKLG	167	181	893.5
	HLA-DQA1*01:02/DQB1*06:02	25.06	GRLSITPAAPSYTLK	165	179	428.1
	HLA-DQA1*05:01/DQB1*03:01	28.02	ITPAAPSYTLKLGEY	169	183	30.9
	HLA-DRB1*15:01	39.16	SITPAAPSYTLKLGE	168	182	658.9
	HLA-DRB1*15:01	41.21	ITPAAPSYTLKLGEY	169	183	815.1
	HLA-DRB1*01:01	41.62	SITPAAPSYTLKLGE	168	182	88.5
	HLA-DRB1*01:01	43.02	ITPAAPSYTLKLGEY	169	183	197
LEGDSCVTI	HLA-DRB1*03:01	2.25	VDLVLEGDSCVTIMS	21	35	197.2
	HLA-DRB1*03:01	2.29	WVDLVLEGDSCVTIM	20	34	247.7
	HLA-DRB1*03:01	2.36	TWVDLVLEGDSCVTI	19	33	471
	HLA-DRB1*03:01	6.08	DLVLEGDSCVTIMSK	22	36	160.3
	HLA-DRB1*03:01	6.21	LVLEGDSCVTIMSKD	23	37	337.6
	HLA-DRB3*01:01	0.28	VDLVLEGDSCVTIMS	21	35	823.8
	HLA-DRB1*04:01	21.95	DLVLEGDSCVTIMSK	22	36	865.1
	HLA-DPA1*03:01/DPB1*04:02	20.93	DLVLEGDSCVTIMSK	22	36	531.4
	HLA-DRB1*13:02	29.15	DLVLEGDSCVTIMSK	22	36	355.9
	HLA-DRB1*13:02	31.31	LVLEGDSCVTIMSKD	23	37	713.4
	HLA-DPA1*03:01/DPB1*04:02	20.82	VDLVLEGDSCVTIMS	21	35	606.8
	HLA-DPA1*03:01/DPB1*04:02	21.61	LVLEGDSCVTIMSKD	23	37	675.5
	HLA-DPA1*03:01/DPB1*04:02	12.78	WVDLVLEGDSCVTIM	20	34	773
	HLA-DPA1*01:03/DPB1*02:01	40.35	TWVDLVLEGDSCVTI	19	33	981.7
	HLA-DPA1*01:03/DPB1*02:01	44.15	WVDLVLEGDSCVTIM	20	34	933.7
	HLA-DQA1*05:01/DQB1*03:01	34.56	WVDLVLEGDSCVTIM	20	34	936.2
	HLA-DPA1*01:03/DPB1*02:01	47.18	VDLVLEGDSCVTIMS	21	35	970.6
	HLA-DPA1*02:01/DPB1*01:01	52.49	DLVLEGDSCVTIMSK	22	36	530.8
	HLA-DPA1*02:01/DPB1*01:01	54.04	LVLEGDSCVTIMSKD	23	37	611.6
	HLA-DPA1*02:01/DPB1*01:01	55.79	VDLVLEGDSCVTIMS	21	35	556.1
LFGGMSWIT	HLA-DQA1*05:01/DQB1*03:01	20.95	GAFRSLFGGMSWIT	447	461	14
	HLA-DQA1*05:01/DQB1*03:01	20.09	GAFRSLFGGMSWITQ	448	462	12.8
	HLA-DQA1*05:01/DQB1*03:01	20.48	AFRSLFGGMSWITQG	449	463	13.1
	HLA-DQA1*05:01/DQB1*03:01	20.53	FRSLFGGMSWITQGL	450	464	13
	HLA-DRB1*04:01	2.87	SLFGGMSWITQGLL	452	466	365.8
	HLA-DQA1*05:01/DQB1*03:01	26.42	SLFGGMSWITQGLL	452	466	25.9
	HLA-DQA1*05:01/DQB1*03:01	21.2	RSLFGGMSWITQGLL	451	465	27.3
	HLA-DQA1*05:01/DQB1*03:01	27.71	LFGGMSWITQGLLGA	453	467	29.8
	HLA-DPA1*01:03/DPB1*02:01	5.68	GAFRSLFGGMSWITQ	448	462	69.1
	HLA-DPA1*01:03/DPB1*02:01	6.58	FRSLFGGMSWITQGL	450	464	67.6
	HLA-DPA1*01:03/DPB1*02:01	5.79	AFRSLFGGMSWITQG	449	463	72.4
	HLA-DPA1*01:03/DPB1*02:01	0.41	RSLFGGMSWITQGLL	451	465	74.5
	HLA-DRB1*15:01	7.86	GAFRSLFGGMSWIT	447	461	174.3
	HLA-DPA1*01/DPB1*04:01	8.94	GAFRSLFGGMSWITQ	448	462	119.5
	HLA-DPA1*01:03/DPB1*02:01	0.42	SLFGGMSWITQGLL	452	466	111.7
	HLA-DRB1*15:01	9.15	GAFRSLFGGMSWITQ	448	462	237.7
	HLA-DPA1*01/DPB1*04:01	10.29	AFRSLFGGMSWITQG	449	463	132.7
	HLA-DPA1*01/DPB1*04:01	10.46	FRSLFGGMSWITQGL	450	464	128.8
	HLA-DPA1*01:03/DPB1*02:01	0.43	LFGGMSWITQGLLGA	453	467	196.8
	HLA-DPA1*01:03/DPB1*02:01	13.22	GAFRSLFGGMSWIT	447	461	131.6
	HLA-DPA1*02:01/DPB1*01:01	0.3	RSLFGGMSWITQGLL	451	465	134.3
	HLA-DRB1*15:01	13.33	AFRSLFGGMSWITQG	449	463	253.7

	HLA-DRB1*15:01	14.28	FRSLFGGMSWITQGL	450	464	233.9
	HLA-DRB1*15:01	15.12	RSLFGGMSWITQGLL	451	465	169.5
	HLA-DPA1*02:01/DPB1*01:01	10.53	FRSLFGGMSWITQGL	450	464	164
	HLA-DPA1*01:01/DPB1*04:01	18.75	GGAFRSLFGGMSWIT	447	461	193.2
	HLA-DPA1*02:01/DPB1*01:01	9.57	AFRSLFGGMSWITQG	449	463	165.3
	HLA-DPA1*02:01/DPB1*01:01	9.54	GAFRSLFGGMSWITQ	448	462	185
	HLA-DRB1*07:01	5.7	GGAFRSLFGGMSWIT	447	461	162.3
	HLA-DRB1*07:01	5.76	GAFRSLFGGMSWITQ	448	462	197.1
	HLA-DRB1*15:01	24.25	SLFGGMSWITQGLLG	452	466	308.1
	HLA-DRB1*07:01	12.45	FRSLFGGMSWITQGL	450	464	269.1
	HLA-DRB1*07:01	12.47	AFRSLFGGMSWITQG	449	463	277.2
	HLA-DPA1*02:01/DPB1*01:01	15.49	GGAFRSLFGGMSWIT	447	461	376.8
	HLA-DPA1*03:01/DPB1*04:02	2.27	RSLFGGMSWITQGLL	451	465	927.2
	HLA-DPA1*03:01/DPB1*04:02	10	FRSLFGGMSWITQGL	450	464	951.8
	HLA-DPA1*03:01/DPB1*04:02	10.98	AFRSLFGGMSWITQG	449	463	994
LHQALAGAI	HLA-DRB1*09:01	0.23	GALHQALAGAIPVEF	260	274	19.9
	HLA-DRB1*09:01	0.24	EGALHQALAGAIPVE	259	273	24.2
	HLA-DRB1*09:01	1.5	ALHQALAGAIPVEFS	261	275	21.8
	HLA-DRB1*09:01	0.25	QEGALHQALAGAIPV	258	272	34.1
	HLA-DRB5*01:01	0.73	EGALHQALAGAIPVE	259	273	11.2
	HLA-DRB1*09:01	0.27	SQEGALHQALAGAIP	257	271	51.9
	HLA-DRB5*01:01	0.73	QEGALHQALAGAIPV	258	272	14.6
	HLA-DRB5*01:01	0.71	GALHQALAGAIPVEF	260	274	15.7
	HLA-DQA1*05:01/DQB1*03:01	14.09	SQEGALHQALAGAIP	257	271	13.7
	HLA-DQA1*05:01/DQB1*03:01	12.61	QEGALHQALAGAIPV	258	272	10.1
	HLA-DQA1*05:01/DQB1*03:01	11.65	EGALHQALAGAIPVE	259	273	8.9
	HLA-DQA1*05:01/DQB1*03:01	10.72	GALHQALAGAIPVEF	260	274	7.2
	HLA-DQA1*05:01/DQB1*03:01	11.47	ALHQALAGAIPVEFS	261	275	6.9
	HLA-DRB1*09:01	0.25	GSQEGALHQALAGAI	256	270	68.6
	HLA-DQA1*05:01/DQB1*03:01	16.59	GSQEGALHQALAGAI	256	270	25
	HLA-DRB5*01:01	0.73	GSQEGALHQALAGAI	256	270	29.6
	HLA-DRB5*01:01	0.78	SQEGALHQALAGAIP	257	271	25.8
	HLA-DRB5*01:01	2.4	ALHQALAGAIPVEFS	261	275	28.2
	HLA-DRB5*01:01	2.46	LHQALAGAIPVEFSS	262	276	56.8
	HLA-DRB1*01:01	6	QEGALHQALAGAIPV	258	272	24.4
	HLA-DRB1*01:01	6	EGALHQALAGAIPVE	259	273	18.7
	HLA-DRB1*01:01	6	GALHQALAGAIPVEF	260	274	20.6
	HLA-DRB1*01:01	6.65	SQEGALHQALAGAIP	257	271	67.9
	HLA-DRB1*01:01	7.08	GSQEGALHQALAGAI	256	270	63.3
	HLA-DRB1*13:02	9.83	GALHQALAGAIPVEF	260	274	444
	HLA-DRB1*07:01	0.75	QEGALHQALAGAIPV	258	272	68.6
	HLA-DQA1*05:01/DQB1*03:01	12.14	LHQALAGAIPVEFSS	262	276	6.7
	HLA-DRB1*13:02	9.69	EGALHQALAGAIPVE	259	273	305.5
	HLA-DRB1*07:01	0.78	GSQEGALHQALAGAI	256	270	90
	HLA-DRB1*13:02	9.69	QEGALHQALAGAIPV	258	272	322.2
	HLA-DRB1*07:01	0.76	GALHQALAGAIPVEF	260	274	98.8
	HLA-DRB1*07:01	0.77	EGALHQALAGAIPVE	259	273	103.3
	HLA-DQA1*01:02/DQB1*06:02	14.6	ALHQALAGAIPVEFS	261	275	221.1
	HLA-DQA1*01:02/DQB1*06:02	15.51	GALHQALAGAIPVEF	260	274	239.2
	HLA-DRB1*07:01	0.81	SQEGALHQALAGAIP	257	271	117.9
	HLA-DRB1*01:01	15.82	LHQALAGAIPVEFSS	262	276	48.4
	HLA-DRB1*07:01	2.43	ALHQALAGAIPVEFS	261	275	127.1
	HLA-DRB1*13:02	10.09	SQEGALHQALAGAIP	257	271	488.6
	HLA-DRB1*13:02	9.75	GSQEGALHQALAGAI	256	270	530.6
	HLA-DRB1*13:02	21.11	ALHQALAGAIPVEFS	261	275	540.5
	HLA-DRB1*07:01	2.47	LHQALAGAIPVEFSS	262	276	171.4
	HLA-DRB1*13:02	21.34	LHQALAGAIPVEFSS	262	276	730
LLGALLWM	HLA-DPA1*01/DPB1*04:01	4.26	SWITQGLLGALLLWM	458	472	328.1
	HLA-DPA1*01/DPB1*04:01	4.37	TQGLLGALLLWMGIN	461	475	498.8
	HLA-DPA1*01/DPB1*04:01	4.74	QGLLGALLLWMGINA	462	476	646.3
	HLA-DPA1*03:01/DPB1*04:02	0.04	SWITQGLLGALLLWM	458	472	43.7
	HLA-DQA1*01:01/DQB1*05:01	0.81	QGLLGALLLWMGINA	462	476	416.1
	HLA-DQA1*01:01/DQB1*05:01	1.06	GLLGALLLWMGINAR	463	477	455.3
	HLA-DQA1*01:01/DQB1*05:01	1.07	LLGALLLWMGINARD	464	478	456.2
	HLA-DQA1*01:01/DQB1*05:01	3.55	ITQGLLGALLLWMGI	460	474	407.2
	HLA-DPA1*03:01/DPB1*04:02	0.05	WITQGLLGALLLWMG	459	473	77.2
	HLA-DQA1*01:01/DQB1*05:01	2.28	TQGLLGALLLWMGIN	461	475	435.2
	HLA-DPA1*03:01/DPB1*04:02	0.05	ITQGLLGALLLWMGI	460	474	80.6
	HLA-DPA1*03:01/DPB1*04:02	0.05	TQGLLGALLLWMGIN	461	475	80.7
	HLA-DPA1*03:01/DPB1*04:02	0.31	GLLGALLLWMGINAR	463	477	92.2

	HLA-DPA1*03:01/DPB1*04:02	0.31	LLGALLLWMGINARD	464	478	92.7
	HLA-DPA1*03:01/DPB1*04:02	0.05	QGLLGALLLWMGINA	462	476	94.1
	HLA-DQA1*01:01/DQB1*05:01	2.94	WITQGLLGALLLWMG	459	473	529.6
	HLA-DQA1*01:02/DQB1*06:02	11.02	LLGALLLWMGINARD	464	478	165.7
	HLA-DQA1*01:01/DQB1*05:01	2.77	SWITQGLLGALLLWM	458	472	746.7
	HLA-DPA1*01:03/DPB1*02:01	1.52	ITQGLLGALLLWMGI	460	474	187.5
	HLA-DPA1*01:03/DPB1*02:01	1.66	SWITQGLLGALLLWM	458	472	192
	HLA-DPA1*01:03/DPB1*02:01	1.56	TQGLLGALLLWMGIN	461	475	227.1
	HLA-DPA1*01:03/DPB1*02:01	1.71	WITQGLLGALLLWMG	459	473	234.8
	HLA-DPA1*01:03/DPB1*02:01	1.99	QGLLGALLLWMGINA	462	476	298.4
	HLA-DPA1*01:03/DPB1*02:01	5.42	GLLGALLLWMGINAR	463	477	453.9
	HLA-DPA1*01:03/DPB1*02:01	7.01	LLGALLLWMGINARD	464	478	687.3
	HLA-DPA1*02:01/DPB1*01:01	1.15	QGLLGALLLWMGINA	462	476	370.7
	HLA-DQA1*05:01/DQB1*03:01	34.24	QGLLGALLLWMGINA	462	476	370.3
	HLA-DPA1*02:01/DPB1*01:01	4.25	LLGALLLWMGINARD	464	478	629.4
	HLA-DQA1*05:01/DQB1*03:01	37.97	GLLGALLLWMGINAR	463	477	471.8
	HLA-DPA1*02:01/DPB1*01:01	3.74	GLLGALLLWMGINAR	463	477	666
	HLA-DQA1*05:01/DQB1*03:01	37.81	LLGALLLWMGINARD	464	478	529.5
LLWMGINA R	HLA-DRB1*04:01	3.21	GALLLWMGINARDRS	466	480	13.6
	HLA-DRB1*04:01	3.32	LGALLLWMGINARDR	465	479	18
	HLA-DRB1*04:01	3.36	ALLLWMGINARDRSI	467	481	13.7
	HLA-DRB1*08:02	3.73	LLLWMGINARDRSIA	468	482	744.5
	HLA-DRB1*04:01	4.1	LLGALLLWMGINARD	464	478	42.3
	HLA-DRB5*01:01	4.75	LLGALLLWMGINARD	464	478	128.3
	HLA-DRB5*01:01	5.26	GLLGALLLWMGINAR	463	477	164.7
	HLA-DRB1*15:01	10.1	LLWMGINARDRSIAL	469	483	48.2
	HLA-DRB1*04:01	7.07	LLLWMGINARDRSIA	468	482	16.9
	HLA-DRB1*04:01	4.19	GLLGALLLWMGINAR	463	477	175.2
	HLA-DRB1*04:05	7.99	GLLGALLLWMGINAR	463	477	303
	HLA-DPA1*03:01/DPB1*04:02	9.18	GALLLWMGINARDRS	466	480	184.2
	HLA-DPA1*03:01/DPB1*04:02	14.28	ALLLWMGINARDRSI	467	481	207.6
	HLA-DPA1*03:01/DPB1*04:02	29.48	LLLWMGINARDRSIA	468	482	317.5
	HLA-DQA1*05:01/DQB1*03:01	39.41	LGALLLWMGINARDR	465	479	731.5
	HLA-DPA1*02:01/DPB1*01:01	15.8	LGALLLWMGINARDR	465	479	857.3
	HLA-DQA1*05:01/DQB1*03:01	40.75	GALLLWMGINARDRS	466	480	771.9
	HLA-DPA1*02:01/DPB1*01:01	30.02	ALLLWMGINARDRSI	467	481	976.2
	HLA-DPA1*02:01/DPB1*01:01	19.63	GALLLWMGINARDRS	466	480	985.1
MSWITQGL L	HLA-DPA1*01/DPB1*04:01	6.77	MSWITQGLLGALLLW	457	471	302.1
	HLA-DPA1*03:01/DPB1*04:02	0.18	FGGMSWITQGLLGAL	454	468	111.2
	HLA-DRB1*15:01	9.92	GGMSWITQGLLGALL	455	469	549.9
	HLA-DRB1*15:01	8.65	GMSWITQGLLGALLL	456	470	548.7
	HLA-DRB1*15:01	8.86	MSWITQGLLGALLLW	457	471	549.1
	HLA-DPA1*01/DPB1*04:01	6.31	GMSWITQGLLGALLL	456	470	311.7
	HLA-DPA1*01/DPB1*04:01	1.34	GGMSWITQGLLGALL	455	469	413.9
	HLA-DPA1*01:03/DPB1*02:01	1.89	MSWITQGLLGALLLW	457	471	217.8
	HLA-DPA1*01/DPB1*04:01	1.32	LFGGMSWITQGLLGA	453	467	440.6
	HLA-DPA1*01:03/DPB1*02:01	2.15	GMSWITQGLLGALLL	456	470	229.4
	HLA-DPA1*01:03/DPB1*02:01	0.4	FGGMSWITQGLLGAL	454	468	231.8
	HLA-DPA1*01:03/DPB1*02:01	0.41	GGMSWITQGLLGALL	455	469	240.3
	HLA-DPA1*02:01/DPB1*01:01	0.23	GGMSWITQGLLGALL	455	469	155.6
	HLA-DPA1*01/DPB1*04:01	1.23	FGGMSWITQGLLGAL	454	468	515.3
	HLA-DRB1*09:01	4.98	RSLFGGMSWITQGGLL	451	465	280.2
	HLA-DPA1*02:01/DPB1*01:01	0.24	FGGMSWITQGLLGAL	454	468	217.1
	HLA-DRB1*07:01	5.86	RSLFGGMSWITQGGLL	451	465	164.2
	HLA-DPA1*02:01/DPB1*01:01	0.31	SLFGGMSWITQGLLG	452	466	243.9
	HLA-DPA1*02:01/DPB1*01:01	0.26	LFGGMSWITQGLLGA	453	467	305.3
	HLA-DRB4*01:01	3.23	MSWITQGLLGALLLW	457	471	401.6
	HLA-DRB1*15:01	24.33	LFGGMSWITQGLLGA	453	467	356.4
	HLA-DRB4*01:01	5.33	FGGMSWITQGLLGAL	454	468	432.4
	HLA-DRB1*09:01	5.09	SLFGGMSWITQGLLG	452	466	490.9
	HLA-DRB1*07:01	6.83	SLFGGMSWITQGLLG	452	466	295.4
	HLA-DRB1*09:01	5.18	LFGGMSWITQGLLGA	453	467	528.1
	HLA-DPA1*03:01/DPB1*04:02	2.17	SLFGGMSWITQGLLG	452	466	764.9
	HLA-DRB1*15:01	29.46	FGGMSWITQGLLGAL	454	468	674.6
	HLA-DRB1*07:01	6.82	LFGGMSWITQGLLGA	453	467	441.6
	HLA-DRB1*07:01	6.72	GMSWITQGLLGALLL	456	470	452.9
	HLA-DRB1*07:01	4.47	GGMSWITQGLLGALL	455	469	558.4
	HLA-DRB1*07:01	6.98	MSWITQGLLGALLLW	457	471	657.8
	HLA-DRB1*07:01	6.35	FGGMSWITQGLLGAL	454	468	757.1

NAKVLIELE	HLA-DQA1*03:01/DQB1*03:02	3.9	ANAKVLIELEPPFGD	367	381	273.6
	HLA-DQA1*04:01/DQB1*04:02	1.97	ANAKVLIELEPPFGD	367	381	363.2
	HLA-DQA1*03:01/DQB1*03:02	3.98	NAKVLIELEPPFGDS	368	382	388
	HLA-DQA1*04:01/DQB1*04:02	3.56	NAKVLIELEPPFGDS	368	382	485.6
	HLA-DRB1*04:05	17.3	VSVATANAKVLIELE	362	376	980.7
	HLA-DPA1*02:01/DPB1*01:01	4.91	ATANAKVLIELEPPF	365	379	451.3
	HLA-DQA1*01:02/DQB1*06:02	29.13	ANAKVLIELEPPFGD	367	381	887.6
	HLA-DPA1*02:01/DPB1*01:01	5.23	VATANAKVLIELEPP	364	378	627.7
	HLA-DPA1*02:01/DPB1*01:01	6.35	VSVATANAKVLIELE	362	376	868.2
	HLA-DPA1*02:01/DPB1*01:01	5.93	SVATANAKVLIELEP	363	377	770.2
	HLA-DRB1*01:01	74.24	ATANAKVLIELEPPF	365	379	815.1
RLVTNPFV	HLA-DRB1*08:02	1.01	PVGRLVTNPFVSV	351	365	168.1
	HLA-DRB1*08:02	0.76	VGRLVTNPFVSVAT	352	366	160.1
	HLA-DRB1*15:01	2.48	VGRLVTNPFVSVAT	352	366	70.3
	HLA-DRB1*15:01	2.64	GRLVTNPFVSVATA	353	367	75.1
	HLA-DRB1*15:01	3.61	RLVTNPFVSVATAN	354	368	67.2
	HLA-DPA1*02:01/DPB1*01:01	2.75	TPVGRLVTNPFVSV	350	364	453.3
	HLA-DPA1*02:01/DPB1*01:01	2.66	PVGRLVTNPFVSV	351	365	354.1
	HLA-DPA1*02:01/DPB1*01:01	2.55	GRLVTNPFVSVATA	353	367	397.1
	HLA-DPA1*02:01/DPB1*01:01	2.65	RLVTNPFVSVATAN	354	368	460.4
	HLA-DRB1*15:01	6.68	PVGRLVTNPFVSV	351	365	86.4
	HLA-DRB1*15:01	6.82	TPVGRLVTNPFVSV	350	364	105.9
	HLA-DRB1*15:01	7.35	LTPVGRLVTNPFVS	349	363	147.8
	HLA-DRB1*09:01	8.74	TPVGRLVTNPFVSV	350	364	638.6
	HLA-DRB1*09:01	9.17	PVGRLVTNPFVSV	351	365	694.7
	HLA-DRB1*09:01	9.65	LTPVGRLVTNPFVS	349	363	589.3
	HLA-DPA1*01:03/DPB1*04:01	0.81	TPVGRLVTNPFVSV	350	364	847.9
	HLA-DPA1*01:03/DPB1*04:01	0.79	PVGRLVTNPFVSV	351	365	678
	HLA-DPA1*01:03/DPB1*04:01	0.79	VGRLVTNPFVSVAT	352	366	665.1
	HLA-DPA1*01:03/DPB1*04:01	0.77	GRLVTNPFVSVATA	353	367	714.6
	HLA-DPA1*01:03/DPB1*04:01	0.93	RLVTNPFVSVATAN	354	368	570
	HLA-DRB1*04:05	14.03	RLVTNPFVSVATAN	354	368	743.8
	HLA-DRB1*15:01	23.91	DLTPVGRLVTNPFV	348	362	212.6
	HLA-DPA1*01:03/DPB1*02:01	0.92	TPVGRLVTNPFVSV	350	364	399.3
	HLA-DRB1*09:01	23.36	DLTPVGRLVTNPFV	348	362	678.7
	HLA-DPA1*02:01/DPB1*01:01	57.28	LTPVGRLVTNPFVS	349	363	940.6
TQGLLGALL	HLA-DQA1*01:02/DQB1*06:02	6.7	SWITQGLLGALLLWM	458	472	175.2
	HLA-DRB1*15:01	8.46	SWITQGLLGALLLWM	458	472	928.2
	HLA-DRB1*04:05	7.81	GGMSWITQGLLGALL	455	469	710.5
	HLA-DRB1*04:05	7.8	GMSWITQGLLGALL	456	470	617.9
	HLA-DRB1*04:05	7.98	MSWITQGLLGALLLW	457	471	651.8
	HLA-DRB1*04:05	6.77	SWITQGLLGALLLWM	458	472	712.1
	HLA-DRB1*04:05	5.75	WITQGLLGALLLWMG	459	473	659.7
	HLA-DPA1*02:01/DPB1*01:01	0.92	MSWITQGLLGALLLW	457	471	100.5
	HLA-DPA1*02:01/DPB1*01:01	1.22	SWITQGLLGALLLWM	458	472	103.5
	HLA-DPA1*02:01/DPB1*01:01	1.09	WITQGLLGALLLWMG	459	473	114
	HLA-DPA1*02:01/DPB1*01:01	1.15	ITQGLLGALLLWMGI	460	474	121.3
	HLA-DQA1*05:01/DQB1*03:01	25.67	SWITQGLLGALLLWM	458	472	76.7
	HLA-DRB1*01:01	5.79	SWITQGLLGALLLWM	458	472	22.9
	HLA-DQA1*05:01/DQB1*03:01	27.91	WITQGLLGALLLWMG	459	473	84.6
	HLA-DQA1*05:01/DQB1*03:01	26.08	MSWITQGLLGALLLW	457	471	92.5
	HLA-DQA1*05:01/DQB1*03:01	30.42	ITQGLLGALLLWMGI	460	474	98.3
	HLA-DPA1*02:01/DPB1*01:01	1.19	TQGLLGALLLWMGIN	461	475	163.6
	HLA-DQA1*05:01/DQB1*03:01	31.83	TQGLLGALLLWMGIN	461	475	119
	HLA-DRB1*01:01	6	WITQGLLGALLLWMG	459	473	40.3
	HLA-DRB1*01:01	10.53	ITQGLLGALLLWMGI	460	474	68.1
	HLA-DRB1*01:01	13.4	TQGLLGALLLWMGIN	461	475	99.6
	HLA-DRB4*01:01	3.26	TQGLLGALLLWMGIN	461	475	429.8
	HLA-DQA1*05:01/DQB1*03:01	25.52	GMSWITQGLLGALL	456	470	98.3
	HLA-DQA1*05:01/DQB1*03:01	25.94	GGMSWITQGLLGALL	455	469	106.4
	HLA-DRB4*01:01	2.65	ITQGLLGALLLWMGI	460	474	530.7
	HLA-DRB4*01:01	2.68	WITQGLLGALLLWMG	459	473	651
	HLA-DRB4*01:01	4.43	SWITQGLLGALLLWM	458	472	761.5
VGGVLLFLS	HLA-DQA1*05:01/DQB1*03:01	19.26	TFLAVGGVLLFLSVN	484	498	24.5
	HLA-DQA1*05:01/DQB1*03:01	16.67	ALTFLAVGGVLLFLS	482	496	25.1
	HLA-DQA1*05:01/DQB1*03:01	18.07	LTFLLAVGGVLLFLSV	483	497	25.2
	HLA-DQA1*01:02/DQB1*06:02	5.49	LTFLLAVGGVLLFLSV	483	497	669.1
	HLA-DQA1*01:02/DQB1*06:02	5.6	ALTFLAVGGVLLFLS	482	496	652.8
	HLA-DQA1*05:01/DQB1*02:01	5.64	ALTFLAVGGVLLFLS	482	496	881.1
	HLA-DQA1*05:01/DQB1*03:01	21.54	FLAVGGVLLFLSVNV	485	499	36.4
	HLA-DQA1*05:01/DQB1*03:01	25.85	LAVGGVLLFLSVNVH	486	500	89.9

	HLA-DPA1*02:01/DPB1*01:01	0.69	FLAVGGVLLFLSVNV	485	499	201.1
	HLA-DQA1*03:01/DQB1*03:02	18.95	LTFLAVGGVLLFLSV	483	497	802.9
	HLA-DQA1*03:01/DQB1*03:02	20.77	TFLAVGGVLLFLSVN	484	498	868.1
	HLA-DQA1*03:01/DQB1*03:02	24.48	FLAVGGVLLFLSVNV	485	499	970
	HLA-DPA1*02:01/DPB1*01:01	0.8	LAVGGVLLFLSVNVH	486	500	358.1
	HLA-DPA1*02:01/DPB1*01:01	0.97	AVGGVLLFLSVNVHA	487	501	413
	HLA-DQA1*05:01/DQB1*03:01	30.3	AVGGVLLFLSVNVHA	487	501	162.2
VKMMNME AA	HLA-DQA1*01:02/DQB1*06:02	1.03	DVKMMNMEANLAEV	42	56	36.1
	HLA-DQA1*01:02/DQB1*06:02	1.03	VKMMNMEANLAEVR	43	57	43.3
	HLA-DRB4*01:01	1.97	VKMMNMEANLAEVR	43	57	46
	HLA-DRB4*01:01	2.02	DVKMMNMEANLAEV	42	56	59.7
	HLA-DRB1*01:01	4.36	TIDVKMMNMEANLA	40	54	9.3
	HLA-DRB4*01:01	0.84	IDVKMMNMEANLAE	41	55	63.2
	HLA-DRB4*01:01	0.83	TIDVKMMNMEANLA	40	54	72.7
	HLA-DRB4*01:01	1.03	PTIDVKMMNMEANL	39	53	77.9
	HLA-DRB4*01:01	1.19	KPTIDVKMMNMEAN	38	52	95.1
	HLA-DQA1*01:02/DQB1*06:02	7.95	IDVKMMNMEANLAE	41	55	33.6
	HLA-DRB1*01:01	6.65	PTIDVKMMNMEANL	39	53	14.5
	HLA-DQA1*01:02/DQB1*06:02	9.3	TIDVKMMNMEANLA	40	54	32.8
	HLA-DRB4*01:01	1.19	DKPTIDVKMMNMEAA	37	51	138.2
	HLA-DQA1*01:02/DQB1*06:02	10.54	PTIDVKMMNMEANL	39	53	35.5
	HLA-DQA1*01:02/DQB1*06:02	12.8	DKPTIDVKMMNMEAA	37	51	55.5
	HLA-DQA1*01:02/DQB1*06:02	12.35	KPTIDVKMMNMEAN	38	52	39.3
	HLA-DRB1*09:01	2.33	TIDVKMMNMEANLA	40	54	177.6
	HLA-DRB1*04:01	12.42	KPTIDVKMMNMEAN	38	52	280.4
	HLA-DRB1*04:01	12.54	DKPTIDVKMMNMEAA	37	51	550.8
	HLA-DRB1*09:01	2.9	PTIDVKMMNMEANL	39	53	273.9
	HLA-DRB1*13:02	38.4	KPTIDVKMMNMEAN	38	52	754.4
	HLA-DRB1*09:01	4.49	KPTIDVKMMNMEAN	38	52	816.3
	HLA-DRB1*01:01	24.9	KPTIDVKMMNMEAN	38	52	62.1
	HLA-DRB1*13:02	43.27	DKPTIDVKMMNMEAA	37	51	946.3
	HLA-DPA1*03:01/DPB1*04:02	15.04	TIDVKMMNMEANLA	40	54	842.9
	HLA-DRB1*01:01	24.9	DKPTIDVKMMNMEAA	37	51	111.1
VLIELEPPF	HLA-DRB3*01:01	0.06	ANAKVLIELEPPFGD	367	381	57.7
	HLA-DRB3*01:01	0.06	NAKVLIELEPPFGDS	368	382	62.1
	HLA-DRB3*01:01	0.06	ATANAKVLIELEPPF	365	379	63.4
	HLA-DRB3*01:01	0.06	TANAKVLIELEPPFG	366	380	67.6
	HLA-DQA1*05:01/DQB1*02:01	3.55	ANAKVLIELEPPFGD	367	381	31.8
	HLA-DQA1*05:01/DQB1*02:01	3.58	TANAKVLIELEPPFG	366	380	36.1
	HLA-DQA1*05:01/DQB1*02:01	4.28	NAKVLIELEPPFGDS	368	382	38
	HLA-DQA1*05:01/DQB1*02:01	5.05	ATANAKVLIELEPPF	365	379	29.7
	HLA-DRB3*01:01	0.06	AKVLIELEPPFGDSY	369	383	141.1
	HLA-DRB3*01:01	0.61	KVLIELEPPFGDSYI	370	384	344.6
	HLA-DRB3*01:01	0.64	VLIELEPPFGDSYIV	371	385	847.7
	HLA-DQA1*05:01/DQB1*02:01	5.98	AKVLIELEPPFGDSY	369	383	41.6
	HLA-DRB1*03:01	0.5	NAKVLIELEPPFGDS	368	382	182.7
	HLA-DRB1*03:01	0.5	TANAKVLIELEPPFG	366	380	771.7
	HLA-DRB1*03:01	0.5	ANAKVLIELEPPFGD	367	381	334.6
	HLA-DRB1*03:01	0.5	AKVLIELEPPFGDSY	369	383	313.4
	HLA-DRB1*03:01	2.13	KVLIELEPPFGDSYI	370	384	502.6
	HLA-DQA1*05:01/DQB1*02:01	11.42	KVLIELEPPFGDSYI	370	384	59.3
	HLA-DRB1*04:05	10.64	ANAKVLIELEPPFGD	367	381	596.2
	HLA-DRB1*04:05	10.64	NAKVLIELEPPFGDS	368	382	632.5
	HLA-DRB1*04:05	11.84	AKVLIELEPPFGDSY	369	383	816.5
	HLA-DRB1*15:01	12.1	AKVLIELEPPFGDSY	369	383	99.4
	HLA-DRB1*15:01	12.15	NAKVLIELEPPFGDS	368	382	102.9
	HLA-DRB1*04:01	8.75	NAKVLIELEPPFGDS	368	382	157.4
	HLA-DRB1*15:01	12.17	ANAKVLIELEPPFGD	367	381	138.9
	HLA-DRB1*04:01	8.9	TANAKVLIELEPPFG	366	380	245.3
	HLA-DRB1*04:01	8.89	ANAKVLIELEPPFGD	367	381	210.1
	HLA-DRB1*04:05	8.61	TANAKVLIELEPPFG	366	380	594.5
	HLA-DRB1*15:01	11.94	TANAKVLIELEPPFG	366	380	188.1
	HLA-DRB1*15:01	16.92	KVLIELEPPFGDSYI	370	384	127.9
	HLA-DRB1*15:01	28.72	VLIELEPPFGDSYIV	371	385	188.2
	HLA-DRB1*04:01	19.22	ATANAKVLIELEPPF	365	379	493.5
	HLA-DRB1*08:02	9.83	NAKVLIELEPPFGDS	368	382	934.9
	HLA-DQA1*05:01/DQB1*02:01	24.98	VLIELEPPFGDSYIV	371	385	99.6
	HLA-DRB1*15:01	23.62	ATANAKVLIELEPPF	365	379	511.9
	HLA-DRB1*04:05	14.63	ATANAKVLIELEPPF	365	379	731.2
	HLA-DPA1*01:03/DPB1*02:01	18.45	NAKVLIELEPPFGDS	368	382	936.8

	HLA-DPA1*02:01/DPB1*01:01	17.2	NAKVLIELEPPFGDS	368	382	488.7
	HLA-DPA1*02:01/DPB1*01:01	9.74	ANAKVLIELEPPFGD	367	381	498.1
	HLA-DPA1*02:01/DPB1*01:01	9.13	TANAKVLIELEPPFG	366	380	512.3
	HLA-DPA1*02:01/DPB1*01:01	26.71	AKVLIELEPPFGDSY	369	383	623.9
	HLA-DPA1*02:01/DPB1*01:01	36.55	KVLIELEPPFGDSYI	370	384	823
VRSYCYLAT	HLA-DRB1*11:01	2.45	LAEVRSYCYLATVSD	53	67	242.1
	HLA-DRB1*11:01	2.5	AEVRSYCYLATVSDL	54	68	266.6
	HLA-DRB1*11:01	1.28	EVRSYCYLATVSDLS	55	69	297.1
	HLA-DPA1*01/DPB1*04:01	5.18	ANLAEVRSYCYLATV	51	65	261.8
	HLA-DPA1*01/DPB1*04:01	5.35	NLAEVRSYCYLATVS	52	66	261.6
	HLA-DPA1*01/DPB1*04:01	5.79	LAEVRSYCYLATVSD	53	67	264.7
	HLA-DPA1*01/DPB1*04:01	6.38	AEVRSYCYLATVSDL	54	68	348.7
	HLA-DRB1*11:01	12.19	NLAEVRSYCYLATVS	52	66	590
	HLA-DPA1*01/DPB1*04:01	7.17	EVRSYCYLATVSDLS	55	69	619.3
	HLA-DPA1*01/DPB1*04:01	14.65	VRSYCYLATVSDLS	56	70	712.3
	HLA-DPA1*01/DPB1*04:01	16.3	AANLAEVRSYCYLAT	50	64	475.4
	HLA-DRB1*04:05	17.9	ANLAEVRSYCYLATV	51	65	609.8
	HLA-DRB1*04:05	18.08	NLAEVRSYCYLATVS	52	66	590.6
	HLA-DRB1*04:05	18.71	AANLAEVRSYCYLAT	50	64	850.7
	HLA-DPA1*03:01/DPB1*04:02	4.7	AEVRSYCYLATVSDL	54	68	333
	HLA-DPA1*03:01/DPB1*04:02	5.62	LAEVRSYCYLATVSD	53	67	411.5
	HLA-DPA1*03:01/DPB1*04:02	5.36	NLAEVRSYCYLATVS	52	66	464.4
	HLA-DPA1*03:01/DPB1*04:02	5.33	ANLAEVRSYCYLATV	51	65	633.3
	HLA-DQA1*01:02/DQB1*06:02	37.91	LAEVRSYCYLATVSD	53	67	692.1
	HLA-DQA1*05:01/DQB1*03:01	42.73	ANLAEVRSYCYLATV	51	65	985
	HLA-DRB1*01:01	50.9	NLAEVRSYCYLATVS	52	66	278.5
WFMDLNLP W	HLA-DRB1*04:01	1.73	HREWFMDLNLPWSSA	214	228	19.9
	HLA-DRB1*04:01	1.65	REWFMDLNLPWSSAG	215	229	24.1
	HLA-DRB1*04:01	1.8	VHREWFMDLNLPWSS	213	227	25.6
	HLA-DRB3*01:01	0.01	FLVHREWFMDLNLPW	211	225	28.3
	HLA-DRB3*01:01	0.01	LVHREWFMDLNLPWS	212	226	28.4
	HLA-DRB3*01:01	0.01	VHREWFMDLNLPWSS	213	227	30
	HLA-DRB1*04:01	1.86	LVHREWFMDLNLPWS	212	226	32.9
	HLA-DRB3*01:01	0.01	HREWFMDLNLPWSSA	214	228	32.2
	HLA-DRB1*03:01	0.21	HREWFMDLNLPWSSA	214	228	38
	HLA-DRB1*11:01	1.44	LVHREWFMDLNLPWS	212	226	262.4
	HLA-DRB1*11:01	1.19	VHREWFMDLNLPWSS	213	227	142.5
	HLA-DRB1*11:01	1.13	HREWFMDLNLPWSSA	214	228	77.4
	HLA-DRB1*11:01	1.11	REWFMDLNLPWSSAG	215	229	103
	HLA-DRB1*04:01	3.19	EWFMDLNLPWSSAGS	216	230	35.7
	HLA-DRB1*03:01	0.21	VHREWFMDLNLPWSS	213	227	43.2
	HLA-DRB1*04:01	3.84	FLVHREWFMDLNLPW	211	225	37.3
	HLA-DRB3*01:01	0.01	REWFMDLNLPWSSAG	215	229	49.1
	HLA-DRB1*11:01	2.84	EWFMDLNLPWSSAGS	216	230	168.9
	HLA-DRB1*11:01	3.46	WFMDLNLPWSSAGST	217	231	259.5
	HLA-DRB3*01:01	0.03	EWFMDLNLPWSSAGS	216	230	79.7
	HLA-DRB1*03:01	0.26	LVHREWFMDLNLPWS	212	226	73.9
	HLA-DRB1*03:01	0.21	REWFMDLNLPWSSAG	215	229	76.7
	HLA-DRB1*04:01	4.93	WFMDLNLPWSSAGST	217	231	62.7
	HLA-DRB1*04:05	4.94	VHREWFMDLNLPWSS	213	227	211.7
	HLA-DRB1*03:01	0.23	FLVHREWFMDLNLPW	211	225	99.4
	HLA-DRB1*04:05	4.99	REWFMDLNLPWSSAG	215	229	325.7
	HLA-DRB1*04:05	5.13	HREWFMDLNLPWSSA	214	228	255.4
	HLA-DRB3*01:01	0.03	WFMDLNLPWSSAGST	217	231	144.9
	HLA-DRB1*03:01	1.05	EWFMDLNLPWSSAGS	216	230	158
	HLA-DRB1*03:01	1.07	WFMDLNLPWSSAGST	217	231	407.4
	HLA-DRB1*11:01	2.01	FLVHREWFMDLNLPW	211	225	488.8
	HLA-DRB1*09:01	7.14	WFMDLNLPWSSAGST	217	231	762.8
	HLA-DRB1*04:05	10.12	EWFMDLNLPWSSAGS	216	230	537.5
	HLA-DRB1*04:05	10.3	WFMDLNLPWSSAGST	217	231	732.4
	HLA-DRB1*15:01	20.86	FLVHREWFMDLNLPW	211	225	106.1
	HLA-DQA1*05:01/DQB1*02:01	10.63	FLVHREWFMDLNLPW	211	225	131.2
	HLA-DQA1*01:01/DQB1*05:01	2.5	EWFMDLNLPWSSAGS	216	230	691.2
	HLA-DQA1*05:01/DQB1*02:01	11.54	LVHREWFMDLNLPWS	212	226	254
	HLA-DRB1*09:01	11.61	REWFMDLNLPWSSAG	215	229	493.5
	HLA-DRB1*09:01	11.69	EWFMDLNLPWSSAGS	216	230	603.4
	HLA-DQA1*05:01/DQB1*02:01	11.92	VHREWFMDLNLPWSS	213	227	328.4
	HLA-DPA1*02:01/DPB1*01:01	5.9	HREWFMDLNLPWSSA	214	228	139.6
	HLA-DQA1*05:01/DQB1*02:01	14.2	HREWFMDLNLPWSSA	214	228	402.1
	HLA-DRB1*15:01	18.66	VHREWFMDLNLPWSS	213	227	160.7

	HLA-DRB1*15:01	16.02	REWFMDLNPWSSAG	215	229	161.6
	HLA-DRB1*15:01	18.03	HREWFMDLNPWSSA	214	228	162.3
	HLA-DRB1*13:02	16.56	HREWFMDLNPWSSA	214	228	645.4
	HLA-DRB1*13:02	16.64	REWFMDLNPWSSAG	215	229	791.7
	HLA-DRB1*13:02	16.68	VHREWFMDLNPWSS	213	227	763.6
	HLA-DRB1*15:01	20.64	LVHREWFMDLNPWS	212	226	214.6
	HLA-DRB1*15:01	19.61	EWFMDLNPWSSAGS	216	230	216.1
	HLA-DPA1*01:03/DPB1*02:01	9.15	HREWFMDLNPWSSA	214	228	379.4
	HLA-DPA1*02:01/DPB1*01:01	5.96	REWFMDLNPWSSAG	215	229	213.8
	HLA-DRB1*15:01	21.69	WFMDLNPWSSAGST	217	231	233.9
	HLA-DQA1*05:01/DQB1*02:01	18.93	REWFMDLNPWSSAG	215	229	494.3
	HLA-DRB1*09:01	19.22	VHREWFMDLNPWSS	213	227	457.8
	HLA-DPA1*01:03/DPB1*02:01	8.46	REWFMDLNPWSSAG	215	229	406.5
	HLA-DRB1*09:01	19.91	HREWFMDLNPWSSA	214	228	402.8
	HLA-DRB1*13:02	21.88	EWFMDLNPWSSAGS	216	230	847.5
	HLA-DQA1*05:01/DQB1*02:01	40.48	EWFMDLNPWSSAGS	216	230	667.9
	HLA-DQA1*05:01/DQB1*02:01	50.63	WFMDLNPWSSAGST	217	231	982.5
	HLA-DPA1*01:03/DPB1*02:01	20.83	EWFMDLNPWSSAGS	216	230	653.2
	HLA-DRB1*09:01	28.7	LVHREWFMDLNPWS	212	226	583.9
	HLA-DPA1*01:03/DPB1*02:01	22.96	WFMDLNPWSSAGST	217	231	979.5
	HLA-DRB1*07:01	28.2	LVHREWFMDLNPWS	212	226	515.7
	HLA-DPA1*02:01/DPB1*01:01	26.68	EWFMDLNPWSSAGS	216	230	634.5
	HLA-DRB1*07:01	20.73	VHREWFMDLNPWSS	213	227	642.8
	HLA-DRB1*07:01	23.51	HREWFMDLNPWSSA	214	228	779.3
	HLA-DRB1*01:01	30.98	HREWFMDLNPWSSA	214	228	210.5
	HLA-DRB1*01:01	28.17	REWFMDLNPWSSAG	215	229	253.7
	HLA-DRB1*09:01	49.36	FLVHREWFMDLNPW	211	225	680.2
	HLA-DRB1*01:01	33.51	VHREWFMDLNPWSS	213	227	453.9
	HLA-DRB1*01:01	43.29	LVHREWFMDLNPWS	212	226	707.5
YLATVSDLS	HLA-DRB1*04:01	0.98	SYCYLATVSDLSTKA	58	72	14.8
	HLA-DRB1*04:01	0.98	YCYLATVSDLSTKAA	59	73	16.5
	HLA-DRB1*04:01	0.98	RSYCYLATVSDLSTK	57	71	21.4
	HLA-DRB1*04:01	1.91	CYLATVSDLSTKAAC	60	74	29.6
	HLA-DRB1*04:01	2.23	YLATVSDLSTKAACP	61	75	33.5
	HLA-DQA1*05:01/DQB1*02:01	3.47	VRSYCYLATVSDLST	56	70	281.9
	HLA-DRB1*11:01	1.25	VRSYCYLATVSDLST	56	70	303.5
	HLA-DRB1*11:01	1.28	RSYCYLATVSDLSTK	57	71	221.4
	HLA-DRB1*11:01	2.03	SYCYLATVSDLSTKA	58	72	126.5
	HLA-DRB1*11:01	1.76	YCYLATVSDLSTKAA	59	73	239.1
	HLA-DQA1*05:01/DQB1*02:01	3.68	EVRSYCYLATVSDLS	55	69	308.7
	HLA-DRB1*07:01	2.95	EVRSYCYLATVSDLS	55	69	38.4
	HLA-DRB1*07:01	2.31	VRSYCYLATVSDLST	56	70	41.6
	HLA-DRB1*04:05	6.48	CYLATVSDLSTKAAC	60	74	80.2
	HLA-DRB1*04:05	7.17	YLATVSDLSTKAACP	61	75	139.7
	HLA-DRB1*01:01	8.28	RSYCYLATVSDLSTK	57	71	10.5
	HLA-DRB1*07:01	2.34	RSYCYLATVSDLSTK	57	71	54.3
	HLA-DQA1*05:01/DQB1*02:01	3.71	RSYCYLATVSDLSTK	57	71	419.9
	HLA-DRB1*01:01	10.18	YCYLATVSDLSTKAA	59	73	12
	HLA-DRB1*08:02	2.03	RSYCYLATVSDLSTK	57	71	979.6
	HLA-DRB1*08:02	1.84	SYCYLATVSDLSTKA	58	72	657.4
	HLA-DRB1*08:02	1.56	YCYLATVSDLSTKAA	59	73	605.7
	HLA-DQA1*05:01/DQB1*02:01	3.96	SYCYLATVSDLSTKA	58	72	618.2
	HLA-DQA1*05:01/DQB1*02:01	6.18	YCYLATVSDLSTKAA	59	73	771.2
	HLA-DRB1*09:01	3.13	RSYCYLATVSDLSTK	57	71	163.8
	HLA-DRB1*01:01	11.07	SYCYLATVSDLSTKA	58	72	8.3
	HLA-DRB1*09:01	3.19	SYCYLATVSDLSTKA	58	72	173.6
	HLA-DRB1*07:01	3.24	SYCYLATVSDLSTKA	58	72	73.6
	HLA-DRB1*09:01	3.15	VRSYCYLATVSDLST	56	70	193.4
	HLA-DRB1*11:01	4.34	CYLATVSDLSTKAAC	60	74	491.1
	HLA-DRB1*11:01	5.06	YLATVSDLSTKAACP	61	75	832.2
	HLA-DRB5*01:01	10.47	RSYCYLATVSDLSTK	57	71	522.7
	HLA-DRB5*01:01	11.04	SYCYLATVSDLSTKA	58	72	480.2
	HLA-DRB5*01:01	11.14	YCYLATVSDLSTKAA	59	73	831
	HLA-DRB1*07:01	3.47	YCYLATVSDLSTKAA	59	73	96.8
	HLA-DPA1*03:01/DPB1*04:02	13.92	CYLATVSDLSTKAAC	60	74	124.9
	HLA-DRB1*08:02	1.67	CYLATVSDLSTKAAC	60	74	620.3
	HLA-DRB1*09:01	3.66	EVRSYCYLATVSDLS	55	69	262.2
	HLA-DRB1*09:01	2.97	YCYLATVSDLSTKAA	59	73	285.6
	HLA-DRB1*01:01	17.82	CYLATVSDLSTKAAC	60	74	24.2
	HLA-DRB1*01:01	21.44	YLATVSDLSTKAACP	61	75	41.8
	HLA-DRB1*07:01	6.68	CYLATVSDLSTKAAC	60	74	278.8

	HLA-DRB1*09:01	7.08	CYLATVSDLSTKAAC	60	74	537.4
	HLA-DPA1*03:01/DPB1*04:02	27.83	YLATVSDLSTKAACP	61	75	353.4
	HLA-DRB1*07:01	10.83	YLATVSDLSTKAACP	61	75	395.3
	HLA-DRB1*15:01	28.8	CYLATVSDLSTKAAC	60	74	619.5
	HLA-DQA1*05:01/DQB1*03:01	30.38	YCYLATVSDLSTKAA	59	73	349.6
	HLA-DQA1*05:01/DQB1*03:01	30.43	EVRSYCYLATVSDLS	55	69	332.7
	HLA-DQA1*05:01/DQB1*03:01	30.9	VRSYCYLATVSDLST	56	70	303.2
	HLA-DQA1*05:01/DQB1*03:01	30.99	SYCYLATVSDLSTKA	58	72	334.1
	HLA-DRB1*15:01	31.19	YLATVSDLSTKAACP	61	75	822.6
	HLA-DQA1*05:01/DQB1*03:01	31.75	RSYCYLATVSDLSTK	57	71	316.7
	HLA-DQA1*05:01/DQB1*03:01	33.07	YLATVSDLSTKAACP	61	75	395.8
	HLA-DQA1*05:01/DQB1*03:01	34.36	CYLATVSDLSTKAAC	60	74	378.9
YVMTVGTK T	HLA-DRB1*09:01	1.26	NAYYVMTVGTKTFLV	199	213	14.4
	HLA-DRB1*07:01	0.26	NAYYVMTVGTKTFLV	199	213	4.8
	HLA-DRB1*07:01	0.29	TNAYYVMTVGTKTFL	198	212	5
	HLA-DRB1*07:01	0.27	AYYVMTVGTKTFLVH	200	214	5.6
	HLA-DRB1*11:01	0.41	IDTNAYYVMTVGTKT	196	210	79.3
	HLA-DRB1*11:01	0.35	DTNAYYVMTVGTKTF	197	211	35.9
	HLA-DRB1*11:01	0.32	TNAYYVMTVGTKTFL	198	212	19.7
	HLA-DRB1*11:01	0.31	NAYYVMTVGTKTFLV	199	213	13.6
	HLA-DRB1*11:01	0.34	AYYVMTVGTKTFLVH	200	214	19.8
	HLA-DRB1*07:01	0.71	YYVMTVGTKTFLVHR	201	215	6.3
	HLA-DRB1*09:01	1.3	AYYVMTVGTKTFLVH	200	214	20.5
	HLA-DRB1*07:01	0.32	DTNAYYVMTVGTKTF	197	211	6.4
	HLA-DRB1*07:01	0.37	IDTNAYYVMTVGTKT	196	210	8.3
	HLA-DRB1*09:01	1.3	TNAYYVMTVGTKTFL	198	212	14.6
	HLA-DRB1*07:01	0.84	YVMTVGTKTFLVHRE	202	216	8.7
	HLA-DRB1*11:01	1.42	YYVMTVGTKTFLVHR	201	215	33.5
	HLA-DRB1*09:01	1.4	IDTNAYYVMTVGTKT	196	210	28.5
	HLA-DRB1*09:01	1.53	DTNAYYVMTVGTKTF	197	211	19.5
	HLA-DRB1*09:01	3.92	YYVMTVGTKTFLVHR	201	215	32.2
	HLA-DRB1*08:02	2.6	NAYYVMTVGTKTFLV	199	213	930.3
	HLA-DRB1*08:02	2.63	AYYVMTVGTKTFLVH	200	214	904.8
	HLA-DRB1*09:01	3.95	YVMTVGTKTFLVHRE	202	216	65.5
	HLA-DRB1*04:01	4.17	NAYYVMTVGTKTFLV	199	213	54.2
	HLA-DRB1*04:01	4.4	TNAYYVMTVGTKTFL	198	212	54.6
	HLA-DRB1*15:01	16.99	DTNAYYVMTVGTKTF	197	211	36.5
	HLA-DRB1*15:01	16.08	TNAYYVMTVGTKTFL	198	212	22.7
	HLA-DRB1*15:01	9.32	NAYYVMTVGTKTFLV	199	213	18
	HLA-DRB1*15:01	9.54	AYYVMTVGTKTFLVH	200	214	24
	HLA-DRB1*15:01	11.68	YYVMTVGTKTFLVHR	201	215	31.3
	HLA-DRB1*15:01	14.33	YVMTVGTKTFLVHRE	202	216	43.8
	HLA-DRB1*01:01	4.57	NAYYVMTVGTKTFLV	199	213	4.9
	HLA-DRB1*04:01	4.64	DTNAYYVMTVGTKTF	197	211	74.2
	HLA-DRB1*04:05	7.88	NAYYVMTVGTKTFLV	199	213	48.4
	HLA-DRB1*04:01	4.98	AYYVMTVGTKTFLVH	200	214	88.3
	HLA-DRB1*01:01	5.2	TNAYYVMTVGTKTFL	198	212	5.5
	HLA-DRB1*01:01	5.2	AYYVMTVGTKTFLVH	200	214	5.8
	HLA-DRB1*04:05	7.98	TNAYYVMTVGTKTFL	198	212	53.6
	HLA-DRB1*01:01	5.79	DTNAYYVMTVGTKTF	197	211	7.3
	HLA-DRB1*04:05	8.3	AYYVMTVGTKTFLVH	200	214	60.9
	HLA-DRB1*03:01	4.17	TNAYYVMTVGTKTFL	198	212	420.9
	HLA-DRB1*03:01	3.96	NAYYVMTVGTKTFLV	199	213	183.3
	HLA-DRB1*03:01	3.97	AYYVMTVGTKTFLVH	200	214	204.3
	HLA-DRB1*01:01	6.42	IDTNAYYVMTVGTKT	196	210	11
	HLA-DRB1*04:01	6.51	IDTNAYYVMTVGTKT	196	210	108.5
	HLA-DRB1*15:01	18.77	IDTNAYYVMTVGTKT	196	210	66.3
	HLA-DRB1*04:05	6.86	IDTNAYYVMTVGTKT	196	210	93.8
	HLA-DRB1*04:05	8.27	DTNAYYVMTVGTKTF	197	211	70.1
	HLA-DRB5*01:01	6.95	YVMTVGTKTFLVHRE	202	216	44.5
	HLA-DRB1*04:01	7.26	YYVMTVGTKTFLVHR	201	215	159.8
	HLA-DRB1*11:01	1.74	YVMTVGTKTFLVHRE	202	216	59.1
	HLA-DRB1*04:05	15.47	YYVMTVGTKTFLVHR	201	215	93.5
	HLA-DRB1*04:05	9.87	YVMTVGTKTFLVHRE	202	216	182
	HLA-DPA1*01:03/DPB1*02:01	10.32	NAYYVMTVGTKTFLV	199	213	368.9
	HLA-DRB1*01:01	12.27	YYVMTVGTKTFLVHR	201	215	7.5
	HLA-DRB1*04:01	12.83	YVMTVGTKTFLVHRE	202	216	289.2
	HLA-DPA1*01/DPB1*04:01	17.71	NAYYVMTVGTKTFLV	199	213	454.4
	HLA-DRB1*01:01	14.48	YVMTVGTKTFLVHRE	202	216	11.8
	HLA-DPA1*02:01/DPB1*01:01	3.88	AYYVMTVGTKTFLVH	200	214	368.6

	HLA-DPA1*02:01/DPB1*01:01	3.94	YYVMTVGTKTFLVHR	201	215	392.2
	HLA-DRB3*01:01	1.41	NAYYVMTVGTKTFLV	199	213	904.3
	HLA-DRB3*01:01	1.48	TNAYYVMTVGTKTFL	198	212	995.1
	HLA-DPA1*01/DPB1*04:01	42.78	TNAYYVMTVGTKTFL	198	212	597
	HLA-DPA1*01/DPB1*04:01	44.75	DTNAYYVMTVGTKTF	197	211	938.7
	HLA-DPA1*03:01/DPB1*04:02	3.51	AYYVMTVGTKTFLVH	200	214	401.3
	HLA-DPA1*03:01/DPB1*04:02	3.24	YYVMTVGTKTFLVHR	201	215	416.7
	HLA-DPA1*03:01/DPB1*04:02	11.98	NAYYVMTVGTKTFLV	199	213	496.9
	HLA-DPA1*03:01/DPB1*04:02	3.23	YVMTVGTKTFLVHRE	202	216	587.5
	HLA-DPA1*01:03/DPB1*02:01	24.39	TNAYYVMTVGTKTFL	198	212	490.6
	HLA-DRB5*01:01	0.76	TNAYYVMTVGTKTFL	198	212	3.5
	HLA-DRB5*01:01	0.75	NAYYVMTVGTKTFLV	199	213	3.7
	HLA-DRB5*01:01	0.86	DTNAYYVMTVGTKTF	197	211	4.5
	HLA-DRB5*01:01	1.46	AYYVMTVGTKTFLVH	200	214	4.9
	HLA-DRB5*01:01	0.91	IDTNAYYVMTVGTKT	196	210	6
	HLA-DRB5*01:01	2.56	YYVMTVGTKTFLVHR	201	215	7.3
	HLA-DRB5*01:01	1.71	GIDTNAYYVMTVGTK	195	209	15.2
	HLA-DPA1*01:03/DPB1*02:01	1.74	AYYVMTVGTKTFLVH	200	214	304.7
	HLA-DPA1*01:03/DPB1*02:01	1.8	YYVMTVGTKTFLVHR	201	215	351.4
	HLA-DRB1*04:01	13.12	GIDTNAYYVMTVGTK	195	209	579.5
	HLA-DRB1*04:05	13.29	GIDTNAYYVMTVGTK	195	209	274.2
	HLA-DPA1*02:01/DPB1*01:01	8.33	NAYYVMTVGTKTFLV	199	213	375.8
	HLA-DPA1*02:01/DPB1*05:01	15.04	NAYYVMTVGTKTFLV	199	213	938.3
	HLA-DPA1*02:01/DPB1*05:01	17.1	AYYVMTVGTKTFLVH	200	214	802.7
	HLA-DPA1*02:01/DPB1*05:01	16.89	YYVMTVGTKTFLVHR	201	215	751.9
	HLA-DRB1*01:01	33.79	GIDTNAYYVMTVGTK	195	209	53.3
	HLA-DPA1*03:01/DPB1*04:02	22.98	TNAYYVMTVGTKTFL	198	212	611.3
	HLA-DPA1*02:01/DPB1*01:01	24.3	TNAYYVMTVGTKTFL	198	212	407.3
	HLA-DPA1*02:01/DPB1*01:01	31.13	IDTNAYYVMTVGTKT	196	210	498.3
	HLA-DQA1*05:01/DQB1*03:01	33.99	NAYYVMTVGTKTFLV	199	213	389.6
	HLA-DQA1*05:01/DQB1*03:01	33.36	IDTNAYYVMTVGTKT	196	210	484.7
	HLA-DQA1*05:01/DQB1*03:01	34.76	TNAYYVMTVGTKTFL	198	212	465.7
	HLA-DPA1*02:01/DPB1*01:01	31.56	DTNAYYVMTVGTKTF	197	211	637.8
MEANLAE V	HLA-DQA1*04:01/DQB1*04:02	0.01	DVKMMNMEANLAEV	56	42	242.9
	HLA-DQA1*01:02/DQB1*06:02	1.05	MMNMEANLAEVRSY	59	45	74.9
	HLA-DQA1*01:02/DQB1*06:02	1.05	KMMNMEANLAEVRS	58	44	77.9
	HLA-DQA1*01:02/DQB1*06:02	1.17	MNMEANLAEVR SYC	60	46	94.4
	HLA-DQA1*01:02/DQB1*06:02	5.52	NMEANLAEVRS YCY	61	47	136.7
	HLA-DQA1*01:02/DQB1*06:02	5.78	MEANLAEVRSY CYL	62	48	175.7
	HLA-DQA1*03:01/DQB1*03:02	3.3	DVKMMNMEAN LAEV	56	42	444.5
	HLA-DQA1*05:01/DQB1*02:01	14.3	KMMNMEANLAE VRS	58	44	580.1
	HLA-DQA1*05:01/DQB1*02:01	14.79	MMNMEANLAEV RSY	59	45	685.2
	HLA-DQA1*04:01/DQB1*04:02	0.27	MEANLAEVRSY CYL	62	48	994.2
	HLA-DQA1*05:01/DQB1*03:01	22.61	KMMNMEANLAE VRS	58	44	53.3
	HLA-DQA1*05:01/DQB1*03:01	22.78	MMNMEANLAEV RSY	59	45	48.7
	HLA-DQA1*05:01/DQB1*03:01	22.91	MNMEANLAEVR SYC	60	46	53.7
	HLA-DQA1*05:01/DQB1*03:01	27.62	NMEANLAEVRS YCY	61	47	147.2
	HLA-DQA1*05:01/DQB1*03:01	30.15	MEANLAEVRSYC YL	62	48	177

* Inhibitory concentration needed to the binding; the lower is the better

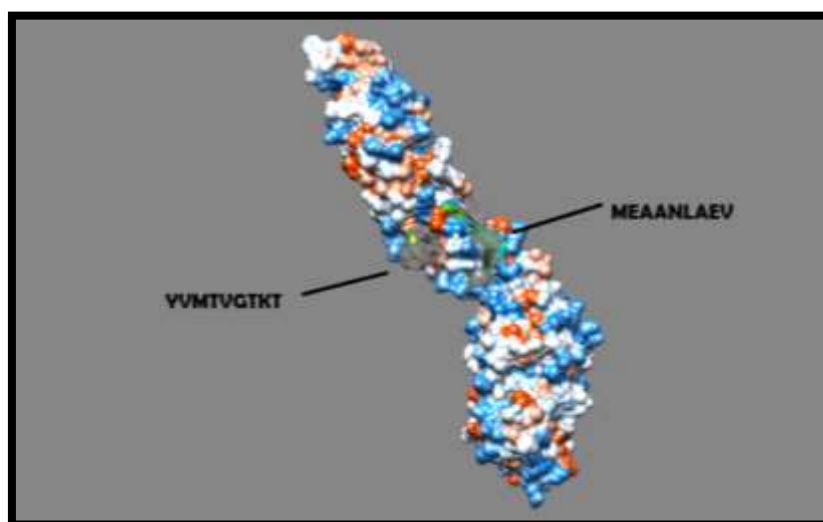


Fig-4: Proposed T-Cell epitopes that interact with MHC Class II

Proposed epitopes of MHC II that are >90% conserved in all international strains in the structural level.

Conservancy analysis

Conservancy tool in IEDB was used to test the conservancy of B cell, MHC I and MHC II epitopes among the 149 retrieved variants. Identity value was set as 100%. All B cell, MHC I and MHC II epitope conservancy results are summarized in the tables (5 - 7).

Table-5: Conservancy analysis of B cell predicted epitopes

Epitope	Epitope length	Percent of protein sequence matches at identity $\geq 100\%$	Minimum identity ¹	Maximum identity ²
FLEGVSGA	8	100.00% (145/145)	100.00%	100.00%
MSKDKPTI	8	98.62% (143/145)	87.50%	100.00%
DLSTKAACPTMGEAHNDKRAPAFV	25	90.34% (131/145)	92.00%	100.00%
VVDRGWGNG	9	100.00% (145/145)	100.00%	100.00%
GLF	3	99.31% (144/145)	66.67%	100.00%
KGSIDT	6	100.00% (145/145)	100.00%	100.00%
PTTVESHGNYSTQVGATQAGRLSITPAAPSYTLK	34	0.69% (1/145)	70.59%	100.00%
YGEVTVDCPRSGIDTN	17	95.86% (139/145)	82.35%	100.00%
PWSSAGSTVWR	11	93.79% (136/145)	54.55%	100.00%
MEFEHPHATKQ	11	95.17% (138/145)	90.91%	100.00%
LGSQEGAL	8	100.00% (145/145)	100.00%	100.00%
PVEFSSNTVKL	11	93.79% (136/145)	81.82%	100.00%
LKGTTYGV	8	100.00% (145/145)	100.00%	100.00%
GTPADTGHGT	10	94.48% (137/145)	90.00%	100.00%
YTGTGDPCKVPIS	13	98.62% (143/145)	92.31%	100.00%
VASLNDLTP	9	100.00% (145/145)	100.00%	100.00%
SVATA	5	97.24% (141/145)	60.00%	100.00%
EPPFGDS	7	100.00% (145/145)	100.00%	100.00%
VGRGEQQINHHWHKSGSSIGKA	22	96.55% (140/145)	95.45%	100.00%
TTTLKG	6	97.93% (142/145)	66.67%	100.00%
AAL	3	100.00% (145/145)	100.00%	100.00%
DTAWDFGSV	9	100.00% (145/145)	100.00%	100.00%
GVFTS	5	98.62% (143/145)	80.00%	100.00%
ARD	3	100.00% (145/145)	100.00%	100.00%

1: the lowest conservancy among variants.

2: the highest conservancy among variants.

Table-6: Conservancy analysis of MHC I predicted epitopes

Epitope	Epitope length	Percent of protein sequence matches at identity $\geq 100\%$	Minimum identity ¹	Maximum identity ²
KTFLVHREW	9	95.86% (139/145)	88.89%	100.00%
REWFMDLNL	9	100.00% (145/145)	100.00%	100.00%
GEQQINHHW	9	97.24% (141/145)	88.89%	100.00%
RSYCYLATV	9	96.55% (140/145)	77.78%	100.00%
RSLFGGMSW	9	99.31% (144/145)	88.89%	100.00%
TPAAPSYTL	9	92.41% (134/145)	66.67%	100.00%

EAANLAEVR	9	97.24% (141/145)	77.78%	100.00%
LEGVSGATW	9	100.00% (145/145)	100.00%	100.00%
WSSAGSTVW	9	93.79% (136/145)	44.44%	100.00%
TTVESHGNY	9	94.48% (137/145)	77.78%	100.00%
GKTKFLVHR	9	95.86% (139/145)	77.78%	100.00%
LAALGDTAW	9	100.00% (145/145)	100.00%	100.00%
AEVRSYCYL	9	98.62% (143/145)	88.89%	100.00%
KAIGRTILK	9	86.21% (125/145)	44.44%	100.00%
DTAWDFGSV	9	100.00% (145/145)	100.00%	100.00%
NARDRSIAL	9	97.24% (141/145)	88.89%	100.00%
TYGVCSKAF	9	96.55% (140/145)	88.89%	100.00%
EVTVDCEPR	9	98.62% (143/145)	88.89%	100.00%
VPISSVASL	9	98.62% (143/145)	88.89%	100.00%
SITPAAPSY	9	95.17% (138/145)	55.56%	100.00%
RLVTVPFV	9	98.62% (143/145)	88.89%	100.00%
RSGIDTNAY	9	97.24% (141/145)	77.78%	100.00%
TFLVHREWF	9	95.86% (139/145)	88.89%	100.00%
GTVVLELQY	9	98.62% (143/145)	88.89%	100.00%
MEFEEPHAT	9	98.62% (143/145)	88.89%	100.00%
GRLVTVPNF	9	98.62% (143/145)	88.89%	100.00%
SVATANAKV	9	96.55% (140/145)	44.44%	100.00%
LTFLAVGGV	9	97.93% (142/145)	88.89%	100.00%
LAVGGVLLF	9	98.62% (143/145)	88.89%	100.00%
CYLATVSDL	9	96.55% (140/145)	77.78%	100.00%
SSAGSTVWR	9	93.79% (136/145)	44.44%	100.00%
TTTLKGAQR	9	97.93% (142/145)	77.78%	100.00%
SGIDTNAYY	9	97.24% (141/145)	77.78%	100.00%
WFMDLNLPW	9	100.00% (145/145)	100.00%	100.00%
QEGALHQAL	9	99.31% (144/145)	88.89%	100.00%
MTVGTKTFL	9	97.24% (141/145)	66.67%	100.00%
VTVPNFVSV	9	97.24% (141/145)	66.67%	100.00%
SLFGGMSWI	9	99.31% (144/145)	88.89%	100.00%
VLLFLSVNV	9	100.00% (145/145)	100.00%	100.00%
RSIALTFLA	9	96.55% (140/145)	88.89%	100.00%
SYTLKLGEY	9	91.72% (133/145)	77.78%	100.00%
KENIKYEVA	9	97.24% (141/145)	88.89%	100.00%
VESHGNYST	9	94.48% (137/145)	77.78%	100.00%
FLVHREWF	9	98.62% (143/145)	88.89%	100.00%
VLIELEPPF	9	99.31% (144/145)	88.89%	100.00%
LPWSSAGST	9	97.93% (142/145)	55.56%	100.00%
SVGGVFTSV	9	98.62% (143/145)	77.78%	100.00%
MEANLAEV	9	97.24% (141/145)	77.78%	100.00%
ATVSDLSTK	9	95.86% (139/145)	77.78%	100.00%
TNAYYVMTV	9	97.24% (141/145)	77.78%	100.00%
TKAIGRTIL	9	86.21% (125/145)	44.44%	100.00%
HQVFGGAFR	9	99.31% (144/145)	88.89%	100.00%
RETLMEFEE	9	98.62% (143/145)	88.89%	100.00%
LAEVRSYCY	9	99.31% (144/145)	88.89%	100.00%
LAGAIPVEF	9	98.62% (143/145)	77.78%	100.00%
TVGKTFLV	9	97.24% (141/145)	66.67%	100.00%
LEGDSCVTI	9	98.62% (143/145)	88.89%	100.00%
GTTYGVCSK	9	96.55% (140/145)	88.89%	100.00%
RADPAFVCR	9	91.03% (132/145)	66.67%	100.00%
FVSVATANA	9	96.55% (140/145)	44.44%	100.00%
ATQAGRLSI	9	0.69% (1/145)	66.67%	100.00%
AGRLSITPA	9	0.69% (1/145)	44.44%	100.00%
LHQALAGAI	9	99.31% (144/145)	88.89%	100.00%
LVLEGDSCV	9	98.62% (143/145)	77.78%	100.00%
ASLNDLTPV	9	100.00% (145/145)	100.00%	100.00%
FLAVGGVLL	9	98.62% (143/145)	88.89%	100.00%
CAKFACSTK	9	97.24% (141/145)	77.78%	100.00%
LLWMGINAR	9	99.31% (144/145)	88.89%	100.00%
TTYGVCSKA	9	96.55% (140/145)	88.89%	100.00%
RVKMEKLQL	9	98.62% (143/145)	88.89%	100.00%
VSVATANAK	9	96.55% (140/145)	44.44%	100.00%
SIALTFLAV	9	97.93% (142/145)	88.89%	100.00%
GIDTNAYYV	9	97.24% (141/145)	77.78%	100.00%
VATANAKVL	9	96.55% (140/145)	55.56%	100.00%
RTILKENIK	9	96.55% (140/145)	66.67%	100.00%
DSCVTIMSK	9	97.93% (142/145)	88.89%	100.00%
STKAACPTM	9	95.17% (138/145)	88.89%	100.00%

QQINHHWHK	9	99.31% (144/145)	88.89%	100.00%
STKAIGRTI	9	85.52% (124/145)	55.56%	100.00%
TVNPFVSVA	9	97.24% (141/145)	55.56%	100.00%
ATKQSVIAL	9	93.79% (136/145)	77.78%	100.00%
AVHQVFGGA	9	98.62% (143/145)	88.89%	100.00%
QVGATQAGR	9	28.28% (41/145)	66.67%	100.00%
LTSGHLKCR	9	100.00% (145/145)	100.00%	100.00%
GMSWITQGL	9	99.31% (144/145)	77.78%	100.00%
LLLWMGINA	9	99.31% (144/145)	88.89%	100.00%
VGKAVHQVF	9	97.24% (141/145)	88.89%	100.00%
MSWITQGLL	9	99.31% (144/145)	77.78%	100.00%
AFKFLGTPA	9	90.34% (131/145)	66.67%	100.00%
QALAGAIPV	9	100.00% (145/145)	100.00%	100.00%
TQVGATQAG	9	28.28% (41/145)	77.78%	100.00%
TVSDLSTKA	9	95.86% (139/145)	77.78%	100.00%
ATANAKVLI	9	96.55% (140/145)	66.67%	100.00%
MMNMEAANL	9	97.24% (141/145)	55.56%	100.00%
LLGALLLWM	9	95.17% (138/145)	88.89%	100.00%
SQEGALHQA	9	99.31% (144/145)	88.89%	100.00%
IKYEVAIFV	9	93.79% (136/145)	88.89%	100.00%
AVGGVLLFL	9	98.62% (143/145)	88.89%	100.00%
WITQGLLGA	9	95.17% (138/145)	77.78%	100.00%
ALHQALAGA	9	99.31% (144/145)	88.89%	100.00%
SVGKAVHQV	9	97.24% (141/145)	88.89%	100.00%
TVWRNRETL	9	93.79% (136/145)	77.78%	100.00%
VHREWFMDL	9	98.62% (143/145)	88.89%	100.00%
SHGNYSTQV	9	28.28% (41/145)	66.67%	100.00%
GHLKCRVKM	9	100.00% (145/145)	100.00%	100.00%

1: the lowest conservancy among variants.

2: the highest conservancy among variants.

Table-7: Conservancy analysis of MHC II predicted epitopes

Epitope	Epitope length	Percent of protein sequence matches at identity $\geq 100\%$	Minimum identity ¹	Maximum identity ²
WMGINARDR	9	97.24% (141/145)	88.89%	100.00%
VLLFLSVNV	9	100.00% (145/145)	100.00%	100.00%
FVSVATANA	9	96.55% (140/145)	44.44%	100.00%
FLAVGGVLL	9	98.62% (143/145)	88.89%	100.00%
LTFLAVGGV	9	97.93% (142/145)	88.89%	100.00%
FKFLGTPAD	9	90.34% (131/145)	66.67%	100.00%
FRSLFGGMS	9	99.31% (144/145)	88.89%	100.00%
HREWFMDLN	9	98.62% (143/145)	88.89%	100.00%
YCYLATVSD	9	96.55% (140/145)	77.78%	100.00%
YYVMTVGTK	9	97.24% (141/145)	77.78%	100.00%
REWFMDLNL	9	100.00% (145/145)	100.00%	100.00%
YVMTVGTKT	9	97.24% (141/145)	66.67%	100.00%
MMNMEAANL	9	97.24% (141/145)	55.56%	100.00%
TANAKVLIE	9	96.55% (140/145)	77.78%	100.00%
ITPAAPSYT	9	95.17% (138/145)	55.56%	100.00%
LAEVRSYCY	9	99.31% (144/145)	88.89%	100.00%
YLATVSDLS	9	96.55% (140/145)	77.78%	100.00%
LFLSVNVHA	9	99.31% (144/145)	88.89%	100.00%
LHQALAGAI	9	99.31% (144/145)	88.89%	100.00%
LGMSNRDFL	9	100.00% (145/145)	100.00%	100.00%
FTTTLKGAQ	9	97.93% (142/145)	77.78%	100.00%
LKGAQRLAA	9	97.93% (142/145)	88.89%	100.00%
ALAGAIPVE	9	99.31% (144/145)	88.89%	100.00%
LLLWMGINA	9	99.31% (144/145)	88.89%	100.00%
WFMDLNLPW	9	100.00% (145/145)	100.00%	100.00%
FTSVGKAVH	9	97.93% (142/145)	88.89%	100.00%
YIVVGRGEQ	9	97.93% (142/145)	88.89%	100.00%
KRADPAFVC	9	95.17% (138/145)	77.78%	100.00%
LLFLSVNVH	9	99.31% (144/145)	88.89%	100.00%
VKLTSGHLK	9	100.00% (145/145)	100.00%	100.00%
IKYEVAIFV	9	93.79% (136/145)	88.89%	100.00%
IGKAFTTTL	9	97.93% (142/145)	77.78%	100.00%
LAGAIPVEF	9	98.62% (143/145)	77.78%	100.00%
VHREWFMDL	9	98.62% (143/145)	88.89%	100.00%
LTPVGRLVT	9	100.00% (145/145)	100.00%	100.00%
NARDRSIAL	9	97.24% (141/145)	88.89%	100.00%

VKMMNMEAA	9	97.24% (141/145)	44.44%	100.00%
KCRVKMEKL	9	99.31% (144/145)	88.89%	100.00%
CSKAFKFLG	9	90.34% (131/145)	77.78%	100.00%
MTVGTKTFL	9	97.24% (141/145)	66.67%	100.00%
FGSVGGVFT	9	98.62% (143/145)	88.89%	100.00%
VGTKTFLVH	9	95.86% (139/145)	77.78%	100.00%
VGRLVTVP	9	100.00% (145/145)	100.00%	100.00%
RLVTVPFV	9	98.62% (143/145)	88.89%	100.00%
VTVPFVSV	9	97.24% (141/145)	66.67%	100.00%
YGEVTVDC	9	97.24% (141/145)	88.89%	100.00%
YGVCSKAFK	9	95.17% (138/145)	88.89%	100.00%
NIKYEVAIF	9	93.79% (136/145)	88.89%	100.00%
LVTVPFVSV	9	98.62% (143/145)	77.78%	100.00%
VNPFVSVAT	9	97.24% (141/145)	44.44%	100.00%
RETLMEFEE	9	98.62% (143/145)	88.89%	100.00%
FLGTPADTG	9	90.34% (131/145)	77.78%	100.00%
LEGDSCVTI	9	98.62% (143/145)	88.89%	100.00%
IFVHGPTTV	9	94.48% (137/145)	88.89%	100.00%
LKCRVKMEK	9	99.31% (144/145)	88.89%	100.00%
RVKMEKLQL	9	98.62% (143/145)	88.89%	100.00%
VTVDCEPRS	9	98.62% (143/145)	88.89%	100.00%
GSVGGVFTS	9	98.62% (143/145)	88.89%	100.00%
VSVATANAK	9	96.55% (140/145)	44.44%	100.00%
NMEAAANLAE	9	97.24% (141/145)	66.67%	100.00%
VWRNRETLM	9	93.79% (136/145)	77.78%	100.00%
LGALLLWMG	9	95.86% (139/145)	88.89%	100.00%
GLLGALLLW	9	95.17% (138/145)	88.89%	100.00%
TFLVHREWF	9	95.86% (139/145)	88.89%	100.00%
WVDLVLEGD	9	98.62% (143/145)	88.89%	100.00%
GHLKCRVKM	9	100.00% (145/145)	100.00%	100.00%
INARDRSIA	9	97.24% (141/145)	88.89%	100.00%
VATANAKVL	9	96.55% (140/145)	55.56%	100.00%
FGGAFRSLF	9	99.31% (144/145)	88.89%	100.00%
MGINARDRS	9	97.24% (141/145)	88.89%	100.00%
PTIDVKMMN	9	97.24% (141/145)	66.67%	100.00%
MSKDKPTID	9	98.62% (143/145)	88.89%	100.00%
SIALTFLAV	9	97.93% (142/145)	88.89%	100.00%
VLIELEPPF	9	99.31% (144/145)	88.89%	100.00%
LMEFEPPHA	9	98.62% (143/145)	88.89%	100.00%
LLWMGINAR	9	99.31% (144/145)	88.89%	100.00%
FSSNTVKLT	9	93.79% (136/145)	77.78%	100.00%
SVATANAKV	9	96.55% (140/145)	44.44%	100.00%
MEAAANLAEV	9	97.24% (141/145)	77.78%	100.00%
VGGVFTSVG	9	98.62% (143/145)	77.78%	100.00%
LFGGMSWIT	9	99.31% (144/145)	88.89%	100.00%
VKMEKLQLK	9	98.62% (143/145)	88.89%	100.00%
ISSVASLND	9	98.62% (143/145)	88.89%	100.00%
MNMEAAANLA	9	97.24% (141/145)	55.56%	100.00%
ALGDTAWDF	9	100.00% (145/145)	100.00%	100.00%
FLVHREWFM	9	98.62% (143/145)	88.89%	100.00%
ETLMEFEPP	9	98.62% (143/145)	88.89%	100.00%
VHQVFGGAF	9	98.62% (143/145)	88.89%	100.00%
NAKVLIELE	9	96.55% (140/145)	88.89%	100.00%
LLGALLLWM	9	95.17% (138/145)	88.89%	100.00%
QGLLGALLL	9	95.17% (138/145)	88.89%	100.00%
FGGMSWITQ	9	99.31% (144/145)	88.89%	100.00%
AFKFLGTPA	9	90.34% (131/145)	66.67%	100.00%
VGGVLLFLS	9	99.31% (144/145)	88.89%	100.00%
SVIALGSQE	9	93.79% (136/145)	88.89%	100.00%
NPFVSVATA	9	97.24% (141/145)	44.44%	100.00%
GHGTVVLEL	9	100.00% (145/145)	100.00%	100.00%
WHKSGSSIG	9	100.00% (145/145)	100.00%	100.00%
VFTSVGKAV	9	97.93% (142/145)	77.78%	100.00%
SQEGALHQA	9	99.31% (144/145)	88.89%	100.00%
FVHGPTTVE	9	94.48% (137/145)	88.89%	100.00%
IPVESSNT	9	93.79% (136/145)	77.78%	100.00%
TILKENIKY	9	96.55% (140/145)	77.78%	100.00%
TLMEFEPPH	9	98.62% (143/145)	88.89%	100.00%
LGSQEGALH	9	99.31% (144/145)	88.89%	100.00%
YTGTDGPCK	9	99.31% (144/145)	88.89%	100.00%
CVTIMSKDK	9	97.93% (142/145)	88.89%	100.00%

GATWVDLVL	9	98.62% (143/145)	88.89%	100.00%
LWMGINARD	9	99.31% (144/145)	88.89%	100.00%
TGHGTVVLE	9	100.00% (145/145)	100.00%	100.00%
LVHREWFMD	9	98.62% (143/145)	88.89%	100.00%
TKQSVIALG	9	93.79% (136/145)	77.78%	100.00%
LNDLTPVGR	9	100.00% (145/145)	100.00%	100.00%
DVKMMNMEA	9	97.93% (142/145)	55.56%	100.00%
KVPISSVAS	9	98.62% (143/145)	88.89%	100.00%
VASLNDLTP	9	100.00% (145/145)	100.00%	100.00%
TVKLTSGHL	9	98.62% (143/145)	88.89%	100.00%
IALTFLAVG	9	97.93% (142/145)	88.89%	100.00%
EAANLAEVR	9	97.24% (141/145)	77.78%	100.00%
TFLAVGGVL	9	98.62% (143/145)	88.89%	100.00%
HGTVVLELQ	9	98.62% (143/145)	88.89%	100.00%
VRSYCYLAT	9	96.55% (140/145)	77.78%	100.00%
SGATWVDLV	9	98.62% (143/145)	88.89%	100.00%
IDTNAYYVM	9	97.24% (141/145)	77.78%	100.00%
SGIDTNAYY	9	97.24% (141/145)	77.78%	100.00%
TQGLLGALL	9	95.17% (138/145)	77.78%	100.00%
MSWITQGLL	9	99.31% (144/145)	77.78%	100.00%
AYYVMTVGT	9	97.24% (141/145)	77.78%	100.00%
WITQGLLGA	9	95.17% (138/145)	77.78%	100.00%
VMTVGTCTF	9	97.24% (141/145)	66.67%	100.00%
IMSKDKPTI	9	98.62% (143/145)	88.89%	100.00%
GGAFRSLFG	9	99.31% (144/145)	88.89%	100.00%
KTFLVHREW	9	95.86% (139/145)	88.89%	100.00%
ILKENIKYE	9	96.55% (140/145)	88.89%	100.00%
FLEGVSGAT	9	100.00% (145/145)	100.00%	100.00%
VEFSSNTVK	9	93.79% (136/145)	77.78%	100.00%
VPISSVASL	9	98.62% (143/145)	88.89%	100.00%
KVLIELEPP	9	97.93% (142/145)	88.89%	100.00%
IDVKMMNME	9	97.24% (141/145)	55.56%	100.00%
KYEVAIFVH	9	95.17% (138/145)	88.89%	100.00%
KAFTTTLKG	9	97.24% (141/145)	77.78%	100.00%
KENIKYEVA	9	97.24% (141/145)	88.89%	100.00%
ITQGLLGAL	9	95.17% (138/145)	77.78%	100.00%
LKENIKYEV	9	96.55% (140/145)	88.89%	100.00%
RDRSIALTF	9	97.24% (141/145)	88.89%	100.00%
ATWVDLVLE	9	98.62% (143/145)	88.89%	100.00%
CYLATVSDL	9	96.55% (140/145)	77.78%	100.00%
AKVLIELEP	9	96.55% (140/145)	88.89%	100.00%
LAVGGVLLF	9	98.62% (143/145)	88.89%	100.00%
TVSDLSTKA	9	95.86% (139/145)	77.78%	100.00%
TTTLKGAQR	9	97.93% (142/145)	77.78%	100.00%
GRTILKENI	9	96.55% (140/145)	66.67%	100.00%
PFVSVATAN	9	97.24% (141/145)	55.56%	100.00%
DSCVTIMSK	9	97.93% (142/145)	88.89%	100.00%
GMSWITQQL	9	99.31% (144/145)	77.78%	100.00%
VSGATWVDL	9	98.62% (143/145)	88.89%	100.00%
EFSSNTVKL	9	93.79% (136/145)	77.78%	100.00%
TWVDLVLEG	9	98.62% (143/145)	88.89%	100.00%
LVLEGDSCV	9	98.62% (143/145)	77.78%	100.00%
GRLVTVNPF	9	98.62% (143/145)	88.89%	100.00%
PWSSAGSTV	9	93.79% (136/145)	44.44%	100.00%
AIFVHGPTT	9	94.48% (137/145)	88.89%	100.00%
FNCLGMSNR	9	100.00% (145/145)	100.00%	100.00%
DRSIALTFL	9	97.24% (141/145)	88.89%	100.00%
EFMDLNLPL	9	100.00% (145/145)	100.00%	100.00%
RTILKENIK	9	96.55% (140/145)	66.67%	100.00%
TTLKGAQRL	9	97.93% (142/145)	77.78%	100.00%
HQVFGGAFR	9	99.31% (144/145)	88.89%	100.00%
RSIALTFLA	9	96.55% (140/145)	88.89%	100.00%
VAIFVHGPT	9	95.17% (138/145)	88.89%	100.00%
NRETLMFEF	9	98.62% (143/145)	88.89%	100.00%
TNAYYVMTV	9	97.24% (141/145)	77.78%	100.00%
CKVPISSVA	9	98.62% (143/145)	88.89%	100.00%
VGKAVHQVF	9	97.24% (141/145)	88.89%	100.00%
WSSAGSTVW	9	93.79% (136/145)	44.44%	100.00%
SAGSTVWRN	9	93.79% (136/145)	44.44%	100.00%
LKLGEYGEV	9	93.79% (136/145)	88.89%	100.00%
VFGGAFRSL	9	98.62% (143/145)	88.89%	100.00%

LEGVSGATW	9	100.00% (145/145)	100.00%	100.00%
ALHQALAGA	9	99.31% (144/145)	88.89%	100.00%
YEVAIFVHG	9	95.17% (138/145)	88.89%	100.00%
LTSGLHKCR	9	100.00% (145/145)	100.00%	100.00%
LIELEPPFG	9	99.31% (144/145)	88.89%	100.00%
TVGKTFLV	9	97.24% (141/145)	66.67%	100.00%
GSIDTCAKF	9	100.00% (145/145)	100.00%	100.00%
EYGEVTVDC	9	97.24% (141/145)	77.78%	100.00%
GTVVLELQY	9	98.62% (143/145)	88.89%	100.00%
MEKLQLKGT	9	98.62% (143/145)	88.89%	100.00%
AEVRSYCYL	9	98.62% (143/145)	88.89%	100.00%
VCSKAFKFL	9	90.34% (131/145)	77.78%	100.00%
QALAGAIPV	9	100.00% (145/145)	100.00%	100.00%
QVFGGAFRS	9	98.62% (143/145)	88.89%	100.00%
KQSVIALGS	9	93.79% (136/145)	77.78%	100.00%
VIALGSQEG	9	93.79% (136/145)	88.89%	100.00%
LKGTTYGVC	9	100.00% (145/145)	100.00%	100.00%
SSIGKAFTT	9	97.93% (142/145)	88.89%	100.00%
IVVGRGEQQ	9	97.93% (142/145)	88.89%	100.00%
HWHKSGSSI	9	100.00% (145/145)	100.00%	100.00%
RSYCYLATV	9	96.55% (140/145)	77.78%	100.00%
EGVSGATWV	9	100.00% (145/145)	100.00%	100.00%
VVLELQYTG	9	98.62% (143/145)	88.89%	100.00%
QLKGTTYGV	9	99.31% (144/145)	88.89%	100.00%
AGAIPVEFS	9	97.93% (142/145)	77.78%	100.00%
AVGGVLLFL	9	98.62% (143/145)	88.89%	100.00%
DKRADPAFV	9	94.48% (137/145)	77.78%	100.00%
AFRSLFGGM	9	99.31% (144/145)	88.89%	100.00%
VHGPTTVES	9	97.93% (142/145)	88.89%	100.00%
TKTFLVHRE	9	95.86% (139/145)	77.78%	100.00%
TVVLELQYT	9	98.62% (143/145)	88.89%	100.00%
GVCSKAFKF	9	95.17% (138/145)	88.89%	100.00%
KLQLKGTTY	9	99.31% (144/145)	88.89%	100.00%
SSVASLNDL	9	98.62% (143/145)	88.89%	100.00%
PEGDSYIVV	9	100.00% (145/145)	100.00%	100.00%
LATVSDLST	9	95.86% (139/145)	77.78%	100.00%
LAALGDTAW	9	100.00% (145/145)	100.00%	100.00%
GIDTNAYYV	9	97.24% (141/145)	77.78%	100.00%
KAACPTMGE	9	95.86% (139/145)	88.89%	100.00%
SLFGGMSWI	9	99.31% (144/145)	88.89%	100.00%
RNRETLMEF	9	98.62% (143/145)	88.89%	100.00%
PISSVASLN	9	98.62% (143/145)	88.89%	100.00%
QEGALHQAL	9	99.31% (144/145)	88.89%	100.00%
EGALHQALA	9	99.31% (144/145)	88.89%	100.00%
PAFVCRQGV	9	91.03% (132/145)	66.67%	100.00%
SLNDLTPVG	9	100.00% (145/145)	100.00%	100.00%
CLGMSNRDF	9	100.00% (145/145)	100.00%	100.00%
WDFGSVGGV	9	98.62% (143/145)	88.89%	100.00%
AKFACSTKA	9	97.24% (141/145)	77.78%	100.00%
KPTIDVKMM	9	97.24% (141/145)	77.78%	100.00%
PHATKQSVI	9	93.79% (136/145)	77.78%	100.00%
TIDVKMMNM	9	97.24% (141/145)	66.67%	100.00%
TSVGKAVHQ	9	97.93% (142/145)	88.89%	100.00%
WRNRETLME	9	98.62% (143/145)	88.89%	100.00%
PVGRLVTVN	9	100.00% (145/145)	100.00%	100.00%
AFTTTLKGA	9	97.93% (142/145)	77.78%	100.00%
NLAEVRSYC	9	99.31% (144/145)	88.89%	100.00%
QQINHHWHK	9	99.31% (144/145)	88.89%	100.00%
INHHWHKSG	9	99.31% (144/145)	88.89%	100.00%
TKAACPTMG	9	95.17% (138/145)	88.89%	100.00%
YTLKLGEYG	9	91.72% (133/145)	77.78%	100.00%
PVEFSNTV	9	93.79% (136/145)	77.78%	100.00%
VCRQGVVDR	9	93.79% (136/145)	88.89%	100.00%
SNTVKLTSG	9	95.86% (139/145)	77.78%	100.00%
LPWSSAGST	9	97.93% (142/145)	55.56%	100.00%
SKAFKFLGT	9	90.34% (131/145)	66.67%	100.00%
ALGSQEGAL	9	100.00% (145/145)	100.00%	100.00%
GALHQALAG	9	99.31% (144/145)	88.89%	100.00%
IALGSQEGA	9	93.79% (136/145)	88.89%	100.00%
EGDSCVTIM	9	97.93% (142/145)	88.89%	100.00%
GLFGKGSID	9	99.31% (144/145)	88.89%	100.00%

ADTGHGTVV	9	100.00% (145/145)	100.00%	100.00%
VVGRGEQQI	9	97.93% (142/145)	88.89%	100.00%
SYIVVGRGE	9	97.93% (142/145)	88.89%	100.00%
VSDLSTKAA	9	97.24% (141/145)	88.89%	100.00%
FEEPHATKQ	9	96.55% (140/145)	88.89%	100.00%
FGKGSIDTC	9	100.00% (145/145)	100.00%	100.00%
VTIMSKDKP	9	97.93% (142/145)	88.89%	100.00%
GINARDRSI	9	97.24% (141/145)	88.89%	100.00%
SDLSTKAAC	9	98.62% (143/145)	88.89%	100.00%
FGDSYIVVG	9	100.00% (145/145)	100.00%	100.00%
GCGLFKGGS	9	99.31% (144/145)	88.89%	100.00%
SWITQGLLG	9	99.31% (144/145)	77.78%	100.00%
RLAALGDTA	9	100.00% (145/145)	100.00%	100.00%
KLGEYGEVT	9	96.55% (140/145)	88.89%	100.00%
GEYGEVTV	9	96.55% (140/145)	77.78%	100.00%
DTCAKFACS	9	97.93% (142/145)	77.78%	100.00%
TYGVCSKAF	9	96.55% (140/145)	88.89%	100.00%
MDLNLPWSS	9	97.93% (142/145)	88.89%	100.00%
KGAQRLAAL	9	99.31% (144/145)	88.89%	100.00%
KLTSGLKLC	9	100.00% (145/145)	100.00%	100.00%
GNGCGLFGK	9	99.31% (144/145)	88.89%	100.00%
GGMSWITQG	9	99.31% (144/145)	88.89%	100.00%
GVSGATWVD	9	100.00% (145/145)	100.00%	100.00%
TLKGAQRLA	9	97.93% (142/145)	88.89%	100.00%
VLELQYTG	9	97.93% (142/145)	88.89%	100.00%
TPVGRVLTV	9	100.00% (145/145)	100.00%	100.00%
LQLKGTYYG	9	99.31% (144/145)	88.89%	100.00%
ARDRSIALT	9	97.24% (141/145)	88.89%	100.00%
DGPCKVPIS	9	99.31% (144/145)	88.89%	100.00%
NCLGMSNRD	9	100.00% (145/145)	100.00%	100.00%
LSTKAACPT	9	95.17% (138/145)	88.89%	100.00%
GDSCVTIMS	9	97.93% (142/145)	88.89%	100.00%
DLNLPWSSA	9	97.93% (142/145)	77.78%	100.00%
AAPSYTLKL	9	93.10% (135/145)	77.78%	100.00%
HHWHKSGSS	9	99.31% (144/145)	88.89%	100.00%
TVESHGNY	9	94.48% (137/145)	77.78%	100.00%
TPAAPSYTL	9	92.41% (134/145)	66.67%	100.00%
SVGKAVHQV	9	97.24% (141/145)	88.89%	100.00%
KAVHQVFEGG	9	98.62% (143/145)	88.89%	100.00%
ATKQSVIAL	9	93.79% (136/145)	77.78%	100.00%
NDLTPVGRL	9	100.00% (145/145)	100.00%	100.00%
AFVCRQGVV	9	91.03% (132/145)	77.78%	100.00%
GKGSIDTCA	9	100.00% (145/145)	100.00%	100.00%
QSVIALGSQ	9	93.79% (136/145)	88.89%	100.00%
SYCYLATVS	9	96.55% (140/145)	77.78%	100.00%
AQRLAALGD	9	100.00% (145/145)	100.00%	100.00%
KSGSSIGKA	9	99.31% (144/145)	88.89%	100.00%
ACPTMGEAH	9	96.55% (140/145)	88.89%	100.00%
TAWDFGSVG	9	100.00% (145/145)	100.00%	100.00%
DLTPVGRLV	9	100.00% (145/145)	100.00%	100.00%
CRVKMEKLQ	9	98.62% (143/145)	88.89%	100.00%
NLPWSSAGS	9	97.93% (142/145)	66.67%	100.00%
VLEGDSCVT	9	98.62% (143/145)	88.89%	100.00%
SVASLNDLT	9	99.31% (144/145)	88.89%	100.00%
FVCRQGVVD	9	91.03% (132/145)	77.78%	100.00%
MEFEEPHAT	9	98.62% (143/145)	88.89%	100.00%
VGRGEQQIN	9	97.93% (142/145)	88.89%	100.00%
ADPAFVCRQ	9	91.03% (132/145)	66.67%	100.00%
TCAKFACST	9	97.93% (142/145)	77.78%	100.00%
SIDTCAKFA	9	98.62% (143/145)	88.89%	100.00%

1: the lowest conservancy among variants.

2: the highest conservancy among variants.

Analysis of the Population Coverage

Epitopes that are suggested interacting with MHC-I and II alleles especially high affinity binding epitopes and that can bind to different set of alleles were selected for population coverage analysis. The

results of population coverage of proposed epitopes are listed in Table (8).

In MHC class I, sex epitopes that interact with most frequent MHC class I alleles (RSYCYLATV, TPAAPSYTL, TVESHGNY, TYGVCSKAF,

MEFEEPHAT and SSAGSTVWR) gave high percentage against the whole world population by IEDB population coverage tool. In MHC class II, two epitopes that interact with most frequent MHC class II alleles

(YVMTVGTKT and MEANLAEV) gave high percentage against the whole world population by IEDB population coverage tool. The population coverage for YVMTVGTKT alone is 99.12%.

Table-8: Population coverage of all epitopes in both MHC class I and II in the world

MHC I		MHC II	
Epitope	Coverage	Epitope	Coverage
RSYCYLATV	46.08%	YVMTVGTKT	99.12%
TPAAPSYTL	27.87%	MEANLAEV	94.55%
TTVESHGNY	12.77%	Epitope set	99.95%
TYGVCSKAF	26.18%		
MEFEEPHAT	10.64%		
SSAGSTVWR	25.64%		
Epitope set	90.38%		

DISCUSSION

Vaccination has conducted great role in protecting millions of people and animals from many various deadly infectious diseases and has been used for more than two centuries [43-44]. Historically, live attenuated or inactivated forms of a wide range of bacterial and viral pathogens have been used for induction of antigen specific responses that protect the host against subsequent infections. Immunity is usually dependent upon a few specific proteins within such fitting, whereas the majority of proteins are dispensable for the induction of protective immunity [45, 46], these proteins may induce allergenic responses, thus intensify the need to eliminate them from vaccine formulations. This has created an interest in peptide vaccines containing only epitopes capable of inducing positive, desirable T cell and B cell mediated immune responses [47].

A variety of methods have been used to identify epitopes in humans. The use of bioinformatics and computational immunology prediction approaches for rapid selection of T and B cell epitope reagents will permit the evaluation of cell mediated responses in the immune pathogenesis of WNV and promote the development of diagnostic reagents, and provide components for epitope based preventive or therapeutic vaccines [48-49].

Epitope specific humoral response is showing considerable progress proven their essential roles for the control of WNV infection *in vivo* [50-51]. Considerable progress has been made towards mapping WNV epitopes within the E protein that have been adapted into candidates for therapeutic uses [52, 53]. In our study, we aimed to determine the highly potential immunogenic epitopes for B and T cells, the prime molecules of cell mediated and humoral immunity, as vaccine candidate for WNV from envelope glycoprotein.

As a result of that the first isolated variant among retrieved strains was collected in 1992 as shown in table (1) we think that the conserved regions among

retrieved strains accompanied with good level of confidence.

Using prediction methods in IEDB of B cell epitope prediction, epitopes should get above threshold scores in Bepipred linear epitope prediction, Emini surface accessibility, and Kolaskar and Tongaonkar antigenicity prediction methods to be considered as potential candidates. According to Table 2; we rapidly identified 24 epitopes of B cell passing the default threshold -0.01 and they are the >90% conserved regions from all retrieved strains of WN virus envelope glycoprotein retrieved. However, only three out of these 24 are observed to overlap the threshold of the three tools; DLSTKAACPTMGEAHNDKRADPAFV, YGEVTVDCPRSGIDTN and PVEFSSNTVKL, and therefore they are candidates for activating B cell humoral response against WN virus. Epitope YGEVTVDCPRSGIDTN was found to have the highest conservancy score as 95.86% among retrieved variants. Mutations in residues S306, K307, T330, and T332 were concluded to reduce or abrogate binding of neutralizing antibodies from several studies [54-56]. Those residues were not found to be part of any proposed B cell epitope, but T330 and T332 are parts of YTGTDGPCKVPIS epitope which does succeed to pass the antigenicity but not the surface accessibility threshold as illustrated in table (2).

Since the immune response of T cell is long lasting response comparing with B cell, where the antigen can easily escape the antibody memory response [57] and CD8+ T and CD4+ T cell responses play a major role in antiviral immunity [58], designing of vaccine against T cell epitope is much more promising. For MHC Class I Alleles prediction, we chose the most common HLA-A, HLA-B and HLA-C alleles to predict their binding affinity to MHC I epitopes [59]. In the study of Kaabinejadian *et al* (2016) the importance of HLA-A2 alleles or protection of transgenic mice from lethal WNV disease was concluded [60]. Study of L. Smith., *et al* was the first to our knowledge to conclude the importance of the same alleles for protection of humans against WNV [61], these studies enforce the need of considering HLA-

A*02 alleles in developing a vaccine against WNV, a HLA-A*02-restricted epitope (430SVGGVFTSV438) from the WNV envelope protein (referred to as E430) in the study of Kim *et al* (2010) was synthesized and observed to activate CD8 cells and protect almost 40% of samples from WNV infection. Although we did not include this highly conserved epitope in the last proposed epitopes to be used in the multi epitope vaccine, a focus need to be targeted to this region. And according to the threshold used in predicting MHC I alleles, this epitope has binding affinity to only HLA-A*68:02 and HLA-A*02:06 as shown in table (3) [62]. Table 3 illustrates 97 T cell highly conserved epitopes predicted to interact with MHC Class I, epitope TPAAPSYTL was found showing high affinity to interact with 5 alleles while RSYCYLATV interacted with 4 alleles including HLA-A*02:01. Considering the study of De Groot *et al.*[2001] which stated the importance of the MHC I allele HLA B*07 [63], the epitope TPAAPSYTL is found to possess binding affinity toward several alleles including HLA B*07 as shown in table (3) increasing its importance. It is to be noted that for efficient induction of either B-cell or cytotoxic T cell responses, the induction of a robust helper T cell response is crucial [64-65].

High coverage percentage in population epitopes that are suggested interacting with MHC-I and II alleles especially high affinity binding epitopes and that can bind to different set of alleles were selected for population coverage analysis. According to Table (8), All proposed MHC I and MHC II epitopes were better chosen to serve the best population coverage percentage as well as the lowest number of peptides to be used as multi epitope vaccine against West Nile Virus infection.

CONCLUSION

Development of a preventive or therapeutic vaccine against this public health threat would be greatly expedited if the correlates of immune response were determined and appropriate components rapidly incorporated into a vaccine. Epitopes defined by methods such as the one described here are likely to contribute substantially to the development of new in vivo and in vitro studies, diagnostics and vaccines for WNV and other emerging infectious diseases.

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Competing interest

The authors declare that they have no competing interests.

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